

SEQUENCE LISTING

<110> Edwards, Jean-Baptiste Dumas Milne
Duclert, Aymeric
Bougueleret, Lydie

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                               Met Lys Lys Val Leu Leu Leu Ile
                               -15                               -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag      161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                               -5                               5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr      209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
                               10                               15                               20
wtg ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att      257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
                               25                               30                               35
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata      305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40                               45                               50                               55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa      354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
                               60                               65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat      414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta      474
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Gly

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ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggctctaatt aattcctctg     180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca     240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg     300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt     357
                                         Met Trp Trp Phe
                                         -20
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cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5
```

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gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1           5           10           15
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gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20           25           30
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aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35           40           45
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aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa      602
Lys
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ctcttcaraa acatgtcttt acaagcatat ctcttgattt gctttctaca ctgttgaatt      662
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gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg      722
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gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw      782
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tttgaaataa aatgatatga gaggtagaca aaaaaaaaaa      822
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<222> 1..21

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score 5.5

seq SFLPSALVIWTS/AF

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Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val

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Ile Trp Thr Ser Ala

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 ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180
 tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
 -35 -30 -25
 aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277
 Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
 -20 -15 -10
 ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg 325
 Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
 -5 1 5 10
 cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc 374
 Pro Asp Asn
 tccaraaggg tttctaaaaa caaaaaaaaaa a 405

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 <222> 1..37
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 1 5 10 15
 Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 20 25 30
 Ser Pro Cys Leu Thr
 35

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 cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag 180
 gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt 231
 Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
 -15 -10 -5
 gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt 279
 Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
 1 5 10
 gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg 327
 Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
 15 20 25
 gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat 375
 Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Arg Arg Asn Tyr
 30 35 40 45
 tct tca gcc tgaaatgaak ccgggatcaa atgggtgctg atcaragccc 424
 Ser Ser Ala
 atattttaaatt tggaaaagtc aaattgasca ttattaaata aagcttggtt aatatgtctc 484
 aaacaaaaaa aa 496

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<222> 1..15
<223> Von Heijne matrix
 score 5.5
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1 5 10 15

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ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
-10 -5 1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
5 10 15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20 25 30 35
Taa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
40 45 50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
55 60 65
atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc 345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
70 75 80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag 393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
85 90 95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg 441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100 105 110 115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc 489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
120 125 130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga 534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
135 140 145
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcaccctc ttggaracaa 594
taaactctca tgcccccaaa aaaaaaaaaa 623

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-10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat 100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
-5 1 5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca 148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
10 15 20 25
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct 196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
30 35 40
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat 244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
45 50 55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt 292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
60 65 70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca 340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
75 80 85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat 388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
90 95 100 105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc 436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
110 115 120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt 484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Phe Gly Val Ile Phe
125 130 135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg 532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp

140	145	150	
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa			580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu			
155	160	165	
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat			628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp			
170	175	180	185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag			676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu			
	190	195	200
gat gag agg ctc acc cct ctc tgaagggctg ttgttctgct tcctcaaraa			727
Asp Glu Arg Leu Thr Pro Leu			
205			
attaaacatt tgtttctgtg tgactgctga gcatcctgaa ataccaagag cagatcatat			787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa			847
c			848

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 1 5 10

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26

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name CMYB_01
score 0.983
sequence tgtcagttg

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<222> complement(18..27)
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name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<221> protein_bind
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<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
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name DELTAEF1_01
score 0.960
sequence gcacacctcag

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<223> matinspector prediction
name GATA_C

score 0.964
sequence agataaatcca

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name CMYB_01
score 0.958
sequence cttcagttg

<221> protein_bind
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name GATA1_02
score 0.959
sequence ttgtagataggaca

<221> protein_bind
<222> 180..190
<223> matinspector prediction
name GATA_C
score 0.953
sequence agataggacat

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1ALPHA47_01
score 0.973
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
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name TAL1BETA47_01
score 0.983
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
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name TAL1BETAITF2_01
score 0.978
sequence cataacagatggtaag

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name MYOD_Q6
score 0.954
sequence accatctgtt

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name GATA1_04
score 0.953

sequence tcaagataaaagta

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score 0.963
sequence agttgggaattcc

<221> protein_bind
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<223> matinspector prediction
name IK2_01
score 0.985
sequence agttgggaattc

<221> protein_bind
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name CREL_01
score 0.962
sequence tgggaattcc

<221> protein_bind
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sequence tcagtgatatggca

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name SRY_02
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sequence taaaacaaaaca

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name E2F_02
score 0.957
sequence tttagcgc

<221> protein_bind
<222> complement(514..521)
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name MZF1_01
score 0.975
sequence tgagggga

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tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta 120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300

atactttatc ttgagtagga gaggcttcct gtggcaacgt ggagaagggg agaggtcgta	360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccggtca tgtgatttag	420
catcagtgat atggcaaagt tgggactaag ggtagtgatc agaggggtaa aattgtgtgt	480
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cttcat	546

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<222> 1..806

<221> transcription start site
<222> 807

<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction
name NFY_Q6
score 0.956
sequence ggaccaatcat

<221> protein_bind
<222> 70..77
<223> matinspector prediction
name MZF1_01

score 0.962
sequence cctggggga

<221> protein_bind
<222> 124..132
<223> matinspector prediction
name CMYB_01
score 0.994
sequence tgaccgttg

<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
name VMYB_02
score 0.985
sequence tccaacggt

<221> protein_bind
<222> 135..143
<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa

<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
name STAT_01
score 0.951
sequence ttccaggaa

<221> protein_bind
<222> complement(252..259)
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name MZF1_01
score 0.956
sequence ttgggggga

<221> protein_bind
<222> 357..368
<223> matinspector prediction
name IK2_01
score 0.965
sequence gaatgggatttc

<221> protein_bind
<222> 384..391
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agaggggga

<221> protein_bind
<222> complement(410..421)
<223> matinspector prediction
name SRY_02
score 0.955

sequence gaaaacaaaaca

<221> protein_bind

<222> 592..599

<223> matinspector prediction

name MZF1_01

score 0.960

sequence gaagggga

<221> protein_bind

<222> 618..627

<223> matinspector prediction

name MYOD_Q6

score 0.981

sequence agcatctgcc

<221> protein_bind

<222> 632..642

<223> matinspector prediction

name DELTAEF1_01

score 0.958

sequence tcccaccttcc

<221> protein_bind

<222> complement(813..823)

<223> matinspector prediction

name S8_01

score 0.992

sequence gaggcaattat

<221> protein_bind

<222> complement(824..831)

<223> matinspector prediction

name MZF1_01

score 0.986

sequence agagggga

<400> 34

tactataggg	cacgcgtggt	cgacggccgg	gctgttcttg	agcagagggc	atgtcagtaa	60
tgattggtcc	ctggggaagg	tctggctggc	tccagcacag	tgaggcattt	aggtatctct	120
cggtgaccgt	tggattcctg	gaagcagtag	ctgttctgtt	tggatctggt	agggacaggg	180
ctcagagggc	taggcacgag	ggaaggtcag	aggagaaggs	aggsarggcc	cagtgaagarg	240
ggagcatgcc	ttcccccaac	cctggcttsc	ycttggyam	agggcgkty	tgggmacttr	300
aaytcagggc	ccaascagaa	scacaggccc	aktcntggct	smaagcacia	tagcctgaat	360
gggatttcag	gttagncagg	gtgagagggg	aggctctctg	gcttagtttt	gttttgtttt	420
ccaaatcaag	gtaacttgct	cccttctgct	acgggccttg	gtcttggtt	gtcctcaccc	480
agtcggaact	ccctaccact	ttcaggagag	tggtttttag	cccgtggggc	tgttctgttc	540
caagcagtgt	gagaacatgg	ctggtagagg	ctctagctgt	gtgcggggcc	tgaaggggag	600
tgggttctcg	cccaaagagc	atctgccc	ttcccacctt	cccttctccc	accagaagct	660
tgcctgagct	gtttggacaa	aaatccaaac	cccacttggc	tactctggcc	tggcttcagc	720
ttggaacca	atacctaggc	ttacaggcca	tcctgagcca	ggggcctctg	gaaattctct	780
tcctgatgg	cctttaggtt	tgggcacaaa	atataattgc	ctctccccct	tcccattttc	840
tctcttgga	gcaatggtca	c				861

<210> 35

<211> 20
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<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 35
ctgggatgga aggcacggta

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 36
gagaccacac agctagacaa

20

<210> 37
<211> 555
<212> DNA
<213> Homo sapiens

<220>
<221> promoter
<222> 1..500

<221> transcription start site
<222> 501

<221> protein_bind
<222> 191..206
<223> matinspector prediction
name ARNT_01
score 0.964
sequence ggactcacgtgctgct

<221> protein_bind
<222> 193..204
<223> matinspector prediction
name NMYC_01
score 0.965
sequence actcacgtgctg

<221> protein_bind
<222> 193..204
<223> matinspector prediction
name USF_01
score 0.985
sequence actcacgtgctg

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name USF_01
score 0.985
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name NMYC_01
score 0.956
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name MYCMAX_02
score 0.972
sequence cagcacgtgagt

<221> protein_bind
<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc

<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga

<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga

<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct

<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc

<221> protein_bind
 <222> complement(460..470)
 <223> matinspector prediction
 name AP1_Q4
 score 0.963
 sequence agtgactgaac

<221> protein_bind
 <222> complement(460..470)
 <223> matinspector prediction
 name AP1FJ_Q2
 score 0.961
 sequence agtgactgaac

<221> protein_bind
 <222> 547..555
 <223> matinspector prediction
 name PADS_C
 score 1.000
 sequence tgtggtctc

<400> 37
 ctatagggca cgcktggtcg acggcccggg ctggtctggt ctgtkgtgga gtcggggttga 60
 aggacagcat ttgtkacatc tggctactcg caccttcct ctgccgtgca cttggccttt 120
 kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga 180
 aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta 240
 gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatacc aagtgattgt 300
 cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag 360
 gttgctctgc ccatgggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc 420
 ggtgtcttct gcctgctccc gctcacatcc cacacttggt ttcagtcact gagttacaga 480
 ttttgctctc tcaatttctc ttgtcttagt cccatcctct gttcccctgg ccagtttgtc 540
 tagctgtgtg gtctc 555

<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 38

ggccatacac ttgagtgac

19

<210> 39

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 39

atatagacaa acgcacacc

19

<210> 40

<211> 568

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 7..471

<221> sig_peptide

<222> 7..99

<223> Von Heijne matrix

score 6.9

seq LLLVPSALSLLLL/LL

<221> polyA_signal

<222> 537..542

<221> polyA_site

<222> 554..568

<400> 40

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gggacc atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct      48
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro
      -30                -25                -20
ctg tcg aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc      96
Leu Ser Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu
      -15                -10                -5
gcc ctc ctc ctg cct cac tgc cag aag ccc ttt gtg tat gac ctt cac      144
Ala Leu Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His
      1                5                10                15
gca gtc aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata      192
Ala Val Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile
      20                25                30
att tgc ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat      240
Ile Cys Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr
      35                40                45
aat ttt agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc      288
Asn Phe Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser
      50                55                60
ttt ttg ctg ggt acc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc      336
Phe Leu Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu
      65                70                75
att gaa gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg      384
Ile Glu Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu
      80                85                90                95
cct tct gga tta atc ttt tgt tgt gct ttt tgc tct gag act aaa ctc      432
Pro Ser Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu
      100               105               110
ttc tta tca aga caa gct atg gca gag aac ttt tcc atc taataaattt      481
Phe Leu Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
      115               120
aagagtagat tcattctgtat gggttgagagt aggctctgac tatgtatatg tgtataataa      541

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acctacatat ccaaaaaaaaa aaaaaaa

568

<210> 41
<211> 569
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 168..332

<221> polyA_signal
<222> 557..562

<400> 41
agggggcggtg gggccatggt ggtcttgctg gcggggaaga agacctttct cccccctctc 60
tgccgcgcct tcgcctgccg cggctgtcaa ctgcctccgg agcgcggcgc cgagcgagg 120
gatacggcgc ccagcggggt cagaaagcaa cattgaatgc agaagaa atg gcg gac 176
Met Ala Asp
1
ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cgc atg tat tat 224
Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg Met Tyr Tyr
5 10 15
aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg gga 272
Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly
20 25 30 35
aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa aag 320
Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys
40 45 50
aag agg agc aac taggagtcca ctctgaccca gccagagtcc aggtttccac 372
Lys Arg Ser Asn
55
aggaagcaga tggagctcct ttcacagggg ctctgagaaa aactggagcc gatctcaaga 432
agccccacat cttcctaagg ggccccatgg cctgtttggg ggagggtag gtcctggggc 492
actgtggggc gcctgcctgc tgatgtgggc tctaggccag cttgttgta cgtacgtgg 552
gtgaaataaa gcccaag 569

<210> 42
<211> 895
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..251

<221> sig_peptide
<222> 51..110
<223> Von Heijne matrix
score 5.3
seq ALIFGGFISLIGA/AF

<221> polyA_signal

<222> 849..854

<221> polyA_site

<222> 882..895

<400> 42

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ccgagagtgc cgggcggtcg gcgggtcagg gcagcccggg gcctgacgcc atg tcc      56
                                   Met Ser
                                   -20
cgg aac ctg cgc acc gcg ctc att ttc ggc ggc ttc atc tcc ctg atc      104
Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile
      -15      -10      -5
ggc gcc gcc ttc tat ccc atc tac ttc cgg ccc cta atg aga ttg gag      152
Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg Leu Glu
      1      5      10
gag tac aag aag gaa caa gct ata aat cgg gct gga att gtt caa gag      200
Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val Gln Glu
      15      20      25      30
gat gtg cag cca cca ggg tta aaa gtg tgg tct gat cca ttt ggc agg      248
Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe Gly Arg
      35      40      45
aaa tgagagggct gtcattcagct ctgattaaga aaggagattt cttcatgctt      301
Lys
tcgattctgc atgggggtaca gccagtcacc tcaccagaga atgacggctg gagaagaaaa      361
ctctgttaata ccataaataa gagtgcttgt aataaaaagac tgtgcacaag gattaatatt      421
tcccttctta agtatcaaaa gaactctgga acaaattata ccattaggaa ggttttcatg      481
attcagttga ttttccaaaa atgaagctat ctcaccacgc tgggttttga ggagcaatct      541
gcttattatt ctgtcggtac cacttactca agcgagctgt gatatgaata caagcaacca      601
gtgggctcgg gaagggtccg gtctcttctg ccattctcca gataagagat ttcagtaaaa      661
gaactgccatg ctgagctgcc ttatagagct cttcgaaaat gttcgagttg ataaagctct      721
ttgaggacaa ggtacttcgt gcacctcatg ctgaagattg caccatgttg gaagataaat      781
atgaagcaag tcaaaactaga tgcatacact tgtgtagaaa tcaataatca attaatagaa      841
gtgaaaaaat agacattaag atgatttatt tccactttgc aaaaaaaaaa aaaa      895

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<210> 43

<211> 691

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 20..613

<221> sig_peptide

<222> 20..82

<223> Von Heijne matrix

score 10

seq LWALAMVTRPASA/AP

<400> 43

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ataccttaga ccctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc      52
                                   Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
                                   -20      -15
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca      100
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro

```

-10	-5	1	5	
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg				148
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu				
10	15	20		
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga tgg				196
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp				
25	30	35		
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa				244
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu				
40	45	50		
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt				292
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu				
55	60	65	70	
cgg gca agc ctg ttg gag act cag atg gag gag gat att ctg cag ctg				340
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu				
75	80	85		
cag gca gag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca cag				388
Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln				
90	95	100		
aag gtg cta cgg gac agc gtg cag cgg cta gaa gtc cag ctg agg agc				436
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser				
105	110	115		
gcc tgg ctg ggc cct gcc tac cga gaa ttt gag gtc tta aag gct cac				484
Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His				
120	125	130		
gct gac aag cag agc cac atc cta tgg gcc ctc aca ggc cac gtg cag				532
Ala Asp Lys Gln Ser His Ile Leu Trp Ala Leu Thr Gly His Val Gln				
135	140	145	150	
cgg cag agg cgg gag atg gtg gca cag cag cat cgg ctg cga cag atc				580
Arg Gln Arg Arg Glu Met Val Ala Gln Gln His Arg Leu Arg Gln Ile				
155	160	165		
cag gag aga ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggaac				633
Gln Glu Arg Leu His Thr Ala Ala Leu Pro Ala				
170	175			
tgaggaccaa tcatgctgca aggaacactt ccacgccccg tgaggcccct gtgcaggg				691

<210> 44

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..416

<221> sig_peptide

<222> 12..86

<223> Von Heijne matrix

score 4

seq LVVMVPLVGLIHL/GW

<221> polyA_signal

<222> 425..430

<221> polyA_site

<222> 445..458

<400> 44

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gctgaagtac t atg agc ctt cgg aac ttg tgg aga gac tac aaa gtt ttg      50
      Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu
      -25                      -20                      -15

gtt gtt atg gtc cct tta gtt ggg ctc ata cat ttg ggg tgg tac aga      98
Val Val Met Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg
      -10                      -5                      1

atc aaa agc agc cct gtt ttc caa ata cct aaa aac gac gac att cct      146
Ile Lys Ser Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro
      5                      10                      15                      20

gag caa gat agt ctg gga ctt tca aat ctt cag aag agc caa atc cag      194
Glu Gln Asp Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln
      25                      30                      35

ggg aag nta gca ggc ttg caa tct tca ggt aaa gaa gca gct ttg aat      242
Gly Lys Xaa Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn
      40                      45                      50

ctg agc ttc ata tcg aaa gaa gag atg aaa aat acc agt tgg att aga      290
Leu Ser Phe Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg
      55                      60                      65

aag aac tgg ctt ctt gta gct ggg ata tct ttc ata ggt gac cat ctt      338
Lys Asn Trp Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu
      70                      75                      80

gga aca tac ttt ttg cag agg tct gca aag cag tct gta aaa ttt cag      386
Gly Thr Tyr Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln
      85                      90                      95                      100

tct caa agc aaa caa aag agt att gaa gag tgaagtaaaa taaatatttg      436
Ser Gln Ser Lys Gln Lys Ser Ile Glu Glu
      105                      110

gaattactaa aaaaaaaaaa aa      458

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<210> 45

<211> 2036

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..1040

<221> sig_peptide

<222> 276..485

<223> Von Heijne matrix

score 3.9

seq SVIGVMLAPFTAG/LS

<221> polyA_site

<222> 2024..2036

<400> 45

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gatcctgggt gcagctcatc acaagcgtcg ggggtgcagca aaaccatcca ggctggacag      60
tggttgga gttccaagaa aagaaacgct tcaccgaaga agtcattgaa tacttccaga      120
agaaagttag ccagtgcat ctgaaaaatcc tgctgactag cgatgaagcc tggaagagat      180
tcgtgcgtgt ggctggattg ccaggggaag aagcagatgc tctctatgaa gctctgaaga      240

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atcttacacc	atatgtggct	attgaggaca	aagac	atg	cag	caa	aaa	gaa	cag	293
				Met	Gln	Gln	Lys	Glu	Gln	
				-70				-65		
cag	ttt	agg	gag	tgg	ttt	ttg	aaa	gag	ttt	341
Gln	Phe	Arg	Glu	Trp	Phe	Leu	Lys	Glu	Phe	
				-60				-55		
att	cag	gag	tcc	ata	gaa	agg	ctt	cgt	gtc	
Ile	Gln	Glu	Ser	Ile	Glu	Arg	Leu	Arg	Val	
				-45				-40		
aag	gtc	cac	aga	ggc	tgc	gtc	atc	gcc	aat	
Lys	Val	His	Arg	Gly	Cys	Val	Ile	Ala	Asn	
				-30				-25		
ggc	atc	ctg	tct	gtc	att	ggc	gtt	atg	ttg	
Gly	Ile	Leu	Ser	Val	Ile	Gly	Val	Met	Leu	
				-15				-10		
ctg	agc	ctg	agc	att	act	gca	gct	ggg	gta	
Leu	Ser	Leu	Ser	Ile	Thr	Ala	Ala	Gly	Val	
1				5				10		
gcc	acg	gct	ggg	atc	gcc	tcc	agc	atc	gtg	
Ala	Thr	Ala	Gly	Ile	Ala	Ser	Ser	Ile	Val	
				20				25		
tca	gca	gaa	ctc	aca	gcc	agc	agg	ctg	act	
Ser	Ala	Glu	Leu	Thr	Ala	Ser	Arg	Leu	Thr	
				35				40		
attg	gag	gca	tta	agg	gac	att	ctg	cat	gac	
Leu	Glu	Ala	Leu	Arg	Asp	Ile	Leu	His	Asp	
				50				55		
tcc	ttt	gca	ctt	gat	ttt	gac	gaa	gcc	aca	
Ser	Phe	Ala	Leu	Asp	Phe	Asp	Glu	Ala	Thr	
65				70				75		
gtc	cat	aca	ctc	agg	aga	tct	aaa	gcc	act	
Val	His	Thr	Leu	Arg	Arg	Ser	Lys	Ala	Thr	
				85				90		
gct	tgg	cga	tat	gta	cct	ata	aat	ggt	ggt	
Ala	Trp	Arg	Tyr	Val	Pro	Ile	Asn	Val	Val	
				100				105		
ggg	gcc	ccc	acc	cgg	ata	gtg	aga	aaa	gta	
Gly	Ala	Pro	Thr	Arg	Ile	Val	Arg	Lys	Val	
				115				120		
gcc	act	tca	ggt	gtc	ctc	ggt	gtg	ctg	gat	
Ala	Thr	Ser	Gly	Val	Leu	Val	Val	Leu	Asp	
				130				135		
gac	tca	ctg	gac	ttg	cac	aag	ggg	gaa	aaa	
Asp	Ser	Leu	Asp	Leu	His	Lys	Gly	Glu	Lys	
				145				150		
ctg	agg	cag	tgg	gct	cag	gag	ctg	gag	gag	
Leu	Arg	Gln	Trp	Ala	Gln	Glu	Leu	Glu	Glu	
				165				170		
cat	atc	cat	cag	agt	cta	aaa	gca	ggc	taggccaat	
His	Ile	His	Gln	Ser	Leu	Lys	Ala	Gly		
				180				185		
agtcaggac	cccaaacgga	gggactggct	gaagccatgg	cagaagaacg	tggattgtga	1120				
agattttcatg	gacattttatt	agttccccc	attaatactt	ttataatttc	ctatgcctgt	1180				
ctttaccgca	atctctaaac	acaaattgtg	aagattttcat	ggacacttat	cacttcccca	1240				
atcaataccc	ttgtgatttc	ttatgcctgt	ctttacttta	atctccta	cctgtcagct	1300				
gaggagggtg	tatgtcacct	caggaccatg	tgataattgc	gttaactgca	caaattgtag	1360				
agcatgtgtg	tttgaacaat	atgaaatctg	ggcaccttga	aaaaagaaca	ggataacagc	1420				

aatcgttcag	gggataagag	agataacctt	aaactctgac	caacagtgag	ccgggtggag	1480
cagagtcata	tttcttttct	ttcaaaagca	aatgggagaa	atatcgctga	attctttttc	1540
tcagcaagga	acatccctga	gaaagagaat	gcaccctga	gggtgggtct	ataaatggcc	1600
tccttgggtg	tggccatctt	ctatggctga	gactgtaggg	atgaaataaa	ccccagtctc	1660
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ccggttgctc	tcaaaaccct	gtctcctgat	aagatgttat	caatgacaat	ggtgcctgaa	1780
acctcattag	caattttaat	ttctccccgg	tcctgtgggc	ctgtgatctc	accctgcctc	1840
cacttgctt	gtgatattct	attaccttgt	gaagtaggtg	atctttgtga	cccacaccct	1900
attcatacac	tccctcccct	tttggaaagtc	cctaataaaa	acttgctggg	tttgcagctt	1960
gtgaggcatc	acggaaccta	ctgatgtgtg	atgtctcccc	tggacaccta	gctttaaaat	2020
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 <213> Homo sapiens

<220>
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 <222> 443..619

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 <222> 443..589
 <223> Von Heijne matrix
 score 7
 seq LICVVCLYIVCRC/GS

<221> polyA_site
 <222> 1267..1276

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cacagctact	gctgcagtag ctggagttgc tttgcattcc acagtacaaa cagcagacta 120
tgtaaaataat	tggtagaaaa attctactct gctgtggaat taccaagata atagagacca 180
gaaactagct	gatcaaatga atgatctcca acaaactgta atgtggctag gggatcatat 240
aggttagttta	gaataatagaa tgcggttaca atgtgattga aatacctctg atttttgcat 300
tactcctcat	ctgtgtaatg aaacagagca tgagtgggaa aaagttaaga gatatttaaa 360
aggtcatact	agaaatttat ctttggatat tgcaaagcta aaggaacaag tatttcaagc 420
ccctcagata	catctgacac ta atg cca gga act gaa gtg ctt gaa gga gct 472
	Met Pro Gly Thr Glu Val Leu Glu Gly Ala
	-45 -40
aca gac gga tta gca gct att aac ctg cta aaa tgg atc aag aca ctt 520	
Thr Asp Gly Leu Ala Ala Ile Asn Leu Leu Lys Trp Ile Lys Thr Leu	
	-35 -30 -25
gga ggc tct gtg att tca atg att gtg ctt tta atc tgt gtt gtt tgt 568	
Gly Gly Ser Val Ile Ser Met Ile Val Leu Leu Ile Cys Val Val Cys	
	-20 -15 -10
ctt tat ata gtc tgt aga tgc gga agc cac ctc tgg aga gaa agc cac 616	
Leu Tyr Ile Val Cys Arg Cys Gly Ser His Leu Trp Arg Glu Ser His	
	-5 1 5
cac tgagagcaag caatgatagc tgtggcgggtt ttgcaaaaag aaaagggaga 669	
His	
10	
caagcgccca gctatagtta ccaataaagc atgggtactgg tattaataaata ggcatgtgtt 729	
ctgttccaat ggaacagaat agagaacca gaaacaaagc caaatattta cagccaactg 789	

atctctgaca	aagcaaacaa	aaacataaag	tggggaaaag	acaccctatt	ccacaaatag	849
tgcagggata	attggcaagc	cacatgtaga	aaaatgaagc	tggatcctcg	tctctcactt	909
tatacaaaaa	tcaactcaa	atgggtcaaa	gtcttaactc	taagacctga	aaccataaca	969
attctagaaa	ataacattgg	aaaaactctt	ctagacattg	gtttaggcaa	aaagttcatg	1029
accaagaacc	caaaagcaa	tgcaataaaa	aggaagataa	atagatggga	cctaattaag	1089
ctgaaaagct	tctgcatagc	aaaaggaata	atcagcagag	caaacagaca	accacaggg	1149
tgggagaaaa	tatttgcaag	ctatgtatct	gacaatggac	taatatccag	aatctacaag	1209
gaattcaaac	aattagcaag	aaaaaacact	tgtatttgt	ttgctctgta	aatcagcaaa	1269
aaaaaaa						1276

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<210> 47
<211> 747
<212> DNA
<213> Homo sapiens
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<222> 206..745
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tggccagttt	tatgaatggc	ttcctgtgtc	taatgacct	gacaacccat	gttcactcaa	120									
gtgccaaaggc	aaaggaacaa	ccctggttgt	tgaactagca	cctaagggtct	tagatgggtac	180									
gcgttgctat	acagaatctt	tggat	atg tgc atc agt	ggg tta tgc caa att		232									
		Met Cys Ile Ser	Gly Leu Cys Gln Ile												
		1		5											
ggt ggc tgc gat cac cag ctg gga agc acc gtc aag gaa gat aac tgt						280									
Val Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys															
10		15		20		25									
ggg gtc tgc aac gga gat ggg tcc acc tgc cgg ctg gtc cga ggg cag						328									
Gly Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln															
		30		35		40									
tat aaa tcc cag ctg tcc gca acc aaa tcg gat gat act gtg gtt gca						376									
Tyr Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala															
		45		50		55									
att ccc tat gga agt aga cat att cgc ctt gtc tta aaa ggt cct gat						424									
Ile Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp															
		60		65		70									
cac tta tat ctg gaa acc aaa acc ctg cag ggg act aaa ggt gaa aac						472									
His Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn															
		75		80		85									
agt ctg agc tcc aca gga act ttc ctt gtg gac aat tct agt gtg gac						520									
Ser Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp															
		90		95		100									
ttc cag aaa ttt cca gac aaa gag ata ctg aga atg gct gga cca ctg						568									
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu															
		110		115		120									
aca gca gat ttc att gtc aag att cgt aac tcg ggc tcc gct gac agt						616									
Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser															
		125		130		135									
aca gtc cag ttc atc ttc tat caa ccc atc atc cac cga tgg agg gag						664									
Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg Trp Arg Glu															
		140		145		150									
acg gat ttc ttt cct tgc tca gca acc tgt gga gga ggt tat cag ctg						712									
Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Gln Leu															

155	160	165	
aca tcg gct gag tgc tac gat ctg agg agc aac cg			747
Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn			
170	175	180	

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<212> DNA
<213> Homo sapiens

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<222> 36..521

<221> sig_peptide
<222> 36..104
<223> Von Heijne matrix
score 7.4
seq VLLLAALPPVLLP/GA

<221> polyA_signal
<222> 528..533
<221> polyA_site
<222> 548..561

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Met Gly Asp Lys Ile Trp	
-20	
ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg	101
Leu Pro Phe Pro Val Leu Leu Ala Ala Leu Pro Pro Val Leu Leu	
-15 -10 -5	
ccct ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt	149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe	
1 5 10 15	
acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg	197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu	
20 25 30	
aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta	245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu	
35 40 45	
gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt	293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe	
50 55 60	
gaa caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt	341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly	
65 70 75	
gat tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag	389
Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys	
80 85 90 95	
gtg att ttc ttt gaa tta atc ccg gat aat atg gga gaa cag gca caa	437
Val Ile Phe Phe Glu Leu Ile Pro Asp Asn Met Gly Glu Gln Ala Gln	
100 105 110	
gaa caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat	485

[illegible]

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<211> 632
<212> DNA
<213> Homo sapiens
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<222> 36..395
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      seq VLLLAALPPVLLP/GA
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599..604
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<221> polyA_site
<222> 619..632
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Met Gly Asp Lys Ile Trp

-20

Ctg ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg 101
Leu Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu

Cct ggg gcg gcc ggc ttc aca cct tcc ctg gat agc gac ttc acc ttt 149
Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe

1 5 10 15

acc ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg 197
Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu
20 25 30

aag gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gga tta 245
Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu
 35 40 45

gat att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt 293
Asp Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe
50 55 60

gaa caa aga aaa tca gat gga gtt cac acg tgt ata aga agt aaa aat 341
Glu Gln Arg Lys Ser Asp Gly Val His Thr Cys Ile Arg Ser Lys Asn
65 70 75

ggg cca ggc act gcg gtt cac gcc tat aat ccc agc act ttc cga ggc 389
Gly Pro Gly Thr Ala Val His Ala Tyr Asn Pro Ser Thr Phe Arg Gly
80 85 90 95

caa gtg tagagactga agttggtgat tacatgttct gctttgacaa tacattcagc 445
Gln Val

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accatttctg agaaggtgat tttctttgaa ttaatcctgg ataatatggg agaacaggca 505
caaggacaag aagattggaa gaaatatatt actggcacag atatattgga tatgaaactg 565
gaagacatcc tggtcagtat ggtcttctaa taaaataaaa attattaaca gccaaaaaaa 625
aaaaaaa 632
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<210> 50
<211> 370
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 21..41
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<222> 328..333
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<221> polyA_site
<222> 357..370
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15																																			

$\begin{matrix} \text{Homo} \\ \text{Pan} \\ \text{Pongo} \\ \text{Gorilla} \\ \text{Orangutan} \end{matrix}$

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<222> 35..160
<223> Von Heijne matrix
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      seq ASLFLLLSLTVFS/IV
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<222> 901..906
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<221> polyA_site
<222> 979..994
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<400> 51

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                               -40
tgg aag gac aag gtt gtt gac ctc ctg tac tgg aga gac att aag aag      103
Trp Lys Asp Lys Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys
-35                               -30                               -25                               -20
act gga gtg gtg ttt ggt gcc agc cta ttc ctg ctg ctt tca ttg aca      151
Thr Gly Val Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr
                               -15                               -10                               -5
gta ttc agc att gtg agc gta aca gcc tac att gcc ttg gcc ctg ctc      199
Val Phe Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu
                               1                               5                               10
tct gtg acc atc agc ttt agg ata tac aag ggt gtg atc caa gct atc      247
Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile
15                               20                               25
cag aaa tca gat gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa      295
Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu
30                               35                               40                               45
gtt gct ata tct gag gag ttg gtt cag aag tac agt aat tct gct ctt      343
Val Ala Ile Ser Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu
                               50                               55                               60
ggg cat gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt      391
Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
65                               70                               75
gat gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt      439
Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
80                               85                               90
acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg gct      487
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala
95                               100                               105
ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat cag gca      535
Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His Gln Ala
110                               115                               120                               125
cag ata gat cat tat cta gta ctt gca aat aag aat gtt aaa gat gct      583
Gln Ile Asp His Tyr Leu Val Leu Ala Asn Lys Asn Val Lys Asp Ala
130                               135                               140
atg gct aaa atc caa gca aaa atc cct gga ttg aag cgc aaa gct gaa      631
Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu
145                               150                               155
tgaaaaacgcc caaaataatt agtaggagtt catctttaa ggggatattc atttgattat      691
acggggggagg gtcagggaag aacgaacctt gacgttgacg tgcagtttca cagatcgttg      751
ttagatcttt atttttagcc atgcactgtt gtgaggaaaa attacctgtc ttgactgcca      811
tgtgttcac atcttaagta ttgtaagctg ctatgtatgg atttaaaccg taatcatatc      871
tttttcctat ctatctgagg cactggtgga ataaaaaacc tgtatatttt actttgttgc      931
agatagtctt gccgcatctt ggcaagttgc agagatggtg gagctagaaa aaaaaaaac      991
aaa

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<210> 52

<211> 412

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 271..399

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gtcactgaga gacgtctcag agaggctgtg cagctgctgg aggactataa gcatgggacc      180
ctgcgccccg gggtcaccaa tgaacagctc tggagtgcac agaaaatcaa gcaggctatt      240
ctacatccgg acaccaatga gaagatcttc atg cca ttt aga atg tca ggt tat      294
                               Met Pro Phe Arg Met Ser Gly Tyr
                               1           5

att cct ttt ggg acg cca att gta agt gtt acc ttc aaa gga ttt cct      342
Ile Pro Phe Gly Thr Pro Ile Val Ser Val Thr Phe Lys Gly Phe Pro
    10           15           20

ttt cta aaa aat tat ttt aaa tgt cta act tta tgt tat tgc tca cgg      390
Phe Leu Lys Asn Tyr Phe Lys Cys Leu Thr Leu Cys Tyr Cys Ser Arg
    25           30           35           40

gta ttt gac tgaattgttg att      412
Val Phe Asp

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<210> 53
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<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 103..252
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<222> 103..213
<223> Von Heijne matrix
      score 3.9
      seq PGPSLRLFSGSQA/SV
<221> polyA_site
<222> 588..597

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gatttggggg ccctgggctc cctagccggc tgcggtgtga ga atg gag tgg gca      114
                               Met Glu Trp Ala
                               -35

gga aag cag cgg gac ttt cag gta agg gca gct ccg ggc tgg gat cat      162
Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro Gly Trp Asp His
      -30           -25           -20

ttg gcc tcc ttt cct ggc cct tct ctc cgg ctg ttt tct ggg agt cag      210
Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe Ser Gly Ser Gln
      -15           -10           -5

gcg agt gtc tgt agt ctc tgc tcg ggg ttt ggg gct cag gaa      252
Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala Gln Glu
    1           5           10

tgatgtcatg ctccaacagt tggattctat tagcttaagg aggagggaaa cagccaattt      312
tcttgacttt gcaaatctag ctgatctcac tcttgctgaa tctgaggtgt ttagacttca      372
ctctaaaaag catcatttta cttttattta gcacaaaggc acaggatatt tttacaggaa      432
gaatctttta tatggaaaaa tctgagttaa catcactccc gtggtgtttg tagttcttac      492
agggaaactc cagtgccttt tgagccgctt gttegtccta gtgaacactg tctgttttgt      552

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597

c	a	c	a	g	t	t	c	c	t	c	t	c	c	a	g	a	c	c	c	c	a	c	c	c	g	g	g	c	g	c
Thr	Val	Pro	Leu	Leu	Leu	Glu	Pro	Ala	Asp	His	Ala	Arg	Gly	Arg	Ala															
1					5				10				15																49	
Cat	gtc	cac	cta	cct	gaa	aat	gtt	cgc	agc	cag	tct	cct	ggc	cat	gtg														97	
His	Val	His	Leu	Pro	Glu	Asn	Val	Arg	Ser	Gln	Ser	Pro	Gly	His	Val															
			20					25				30																		
cgc	agg	ggc	aga	agt	ggt	gca	cag	gta	cta	ccg	acc	gga	cct	gat	gag														145	
Arg	Arg	Gly	Arg	Ser	Gly	Ala	Gln	Val	Leu	Pro	Thr	Gly	Pro	Asp	Glu															
		35				40					45																			
aaa	cag	ggt	gag	aag	agt	gaa	ggt	gat	ttc	tca	aag	tca	cat	agc	tta														193	
Lys	Gln	Val	Glu	Lys	Ser	Glu	Val	Asp	Phe	Ser	Lys	Ser	His	Ser	Leu															
	50					55					60																			
gtg	aga	cga	ttt	gag	gat	ctg	aag	ccc	aag	ctt	tct	ggt	tgc	aaa	act														241	
Val	Arg	Arg	Phe	Glu	Asp	Leu	Lys	Pro	Lys	Leu	Ser	Val	Cys	Lys	Thr															
65					70				75				80																	
gga	tca	caa	gtc	ttt	cgg	tcg	gag	aac	tgg	aag	gtc	tgg	gca	gag	tcg														289	
Gly	Ser	Gln	Val	Phe	Arg	Ser	Glu	Asn	Trp	Lys	Val	Trp	Ala	Glu	Ser															
			85				90				95																			
agc	aga	gga	gac	cat	gat	gac	tgc	cta	gac	ttg	tgc	tca	gtg	ctg	tgt														337	
Ser	Arg	Gly	Asp	His	Asp	Asp	Cys	Leu	Asp	Leu	Cys	Ser	Val	Leu	Cys															
		100				105					110																			
tgg	gga	gaa	ctg	cta	cgg	aca	ata	cct	gaa	att	cca	cca	aag	cgt	gga														385	
Trp	Gly	Glu	Leu	Leu	Arg	Thr	Ile	Pro	Glu	Ile	Pro	Pro	Lys	Arg	Gly															
		115				120					125																			
gaa	ctc	aaa	acg	gag	ctt	ttg	gga	ctg	aaa	gaa	aga	aaa	cac	aaa	cct														433	
Glu	Leu	Lys	Thr	Glu	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Lys	His	Lys	Pro															
	130				135																									

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 <213> Homo sapiens

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 <222> 769..774

<221> polyA_site
 <222> 690..703

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ctc agc cct gct aag ctg atg atg ctg act ata gga gat gtt att aaa      102
Leu Ser Pro Ala Lys Leu Met Met Leu Thr Ile Gly Asp Val Ile Lys
      10       15       20
caa ctg att gaa gcc cac gag cag ggg aaa gac atc gat cta aat aag      150
Gln Leu Ile Glu Ala His Glu Gln Gly Lys Asp Ile Asp Leu Asn Lys
      25       30       35       40
gtg aga acc aag aca gct gcc aaa tat ggc ctt tct gcc cag ccc cgc      198
Val Arg Thr Lys Thr Ala Ala Lys Tyr Gly Leu Ser Ala Gln Pro Arg
      45       50       55
ctg gtg gat atc att gct gcc gtc cct cct gag tagctgggat tacaggcacc      251
Leu Val Asp Ile Ile Ala Ala Val Pro Pro Glu
      60       65
cgccgctgcc aatttttcta ttttttagtag ggatgggggt ttcaccatat tggtcaggct      311
ggtctcgaac tcctgacctc aggtgatcaa cccaccttgg cctccctaaa tgccgggatt      371
acaggcatga gccaccgctc cgggcctttg attttttaag gtggattttg gttgttataa      431
atggagaaag gtaagagttc aagttcaacc cgtgtgtgaa agcaaaacaa tggaaaacag      491
gattggcttc ttcaaaggct cctctttaga aactgcctct ttgaaatttc gaggtaatct      551
acttttgaga ctctgcctgg agaggggtcag ttcctaagtt aaaagcatcg cttaaccttg      611
gctcctgtgg cattttacaa aggttttaaag gaattgattc ctctgaaagg gcctgaaaat      671
aaaaagtctt taacatacaa aaaaaaaaaa aa                                703
  
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 <212> DNA
 <213> Homo sapiens

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<221> polyA_signal
 <222> 694..699

<221> polyA_site
 <222> 713..725


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cagggccggc cccacgtcct ctgcgcacca cctcagattg gatcctctgt gcgccacccc      120
tgagttggat ccagggctag ctgctgttga cctccccact cccacgctgc cctcctgcct      180
gcagccatga cgccctgct caccctgacg ctgggtgggtcc tcatgggctt acctctggcc      240
caggccttgg actgccacgt gtgaggacta caaatccctc caggatatca ttgccatcct      300
gggt atg gat gaa ctt tct gag gaa gac aag ttg acc gtg tcc cgt gca      349
    Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala
      1          5          10          15

cgg aaa ata cag cgt ttc ttg tct cag cca ttc cag gtt gct gag gtc      397
Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val
      20          25          30

ttc aca ggt cat atg ggg aag ctg gta ccc ctg aag gag acc atc aaa      445
Phe Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys
      35          40          45

gga ttc cag cag att ttg gca ggt gaa tat gac cat ctc cca gaa cag      493
Gly Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln
      50          55          60

gcc ttc tat atg gtg gga ccc att gaa gaa gct gtg gca aaa gct gat      541
Ala Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp
      65          70          75

aaag ctg gct gaa gag cat tca tcg tgaggggtct ttgtcctctg tactgtctct      595
Lys Leu Ala Glu Glu His Ser Ser
      80          85

ctccttgccc ctaacccaaa aagcttcatt tttctgtgta ggctgcacaa gagccttgat      655
tgaagatata ttctttctga acagtattta aggtttccaa taaagtgtac acccctcaaa      715
aaaaaaaaaa      725

<210> 57
<211> 1705
<212> DNA
<213> Homo sapiens

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<222> 124..873

<221> sig_peptide
<222> 124..378
<223> Von Heijne matrix
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<222> 1673..1678

<221> polyA_site
<222> 1694..1705

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cccgcagagc ctgaccaggg ctctggacat cctgagccca agtccccac actcagtgca      120
gtg atg agt gcg gaa gtg aag gtg aca ggg cag aac cag gag caa ttt      168
    Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe

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-85	-80	-75	
ctg ctc cta gcc aag tgc gcc aag ggg gca gcg ctg gcc aca ctc atc			216
Leu Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile			
-70	-65	-60	-55
cat cag gtg ctg gag gcc cct ggt gtc tac gtg ttt gga gaa ctg ctg			264
His Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu			
-50	-45	-40	
gac atg ccc aat gtt aga gag ctg naa gcc cgg aat ctt cct cca cta			312
Asp Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu			
-35	-30	-25	
aca gag gct cag aag aat aag ctt cga cac ctc tca gtt gtc acc ctg			360
Thr Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu			
-20	-15	-10	
gct gct aaa gta aag tgt atc cca tat gca gtg ttg ctg gag gct ctt			408
Ala Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu			
-5	1	5	10
gcc ctg cgt aat gtg cgg cag ctg gaa gac ctt gtg att gag gct gtg			456
Ala Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val			
15	20	25	
tat gct gac gtg ctt cgt ggc tcc ctg gac cag cgc aac cag cgg ctc			504
Tyr Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu			
30	35	40	
gag gtt gac tac agc atc ggg cgg gac atc cag cgc cag gac ctc agt			552
Glu Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser			
45	50	55	
gcc att gcc cga acc ctg cag gaa tgg tgt gtg ggc tgt gag gtc gtg			600
Ala Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val			
60	65	70	
ctg tca ggc att gag gag cag gtg agc cgt gcc aac caa cac aag gag			648
Leu Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu			
75	80	85	90
cag cag ctg ggc ctg aag cag cag att gag agt gag gtt gcc aac ctt			696
Gln Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu			
95	100	105	
aaa aaa acc att aaa gtt acg acg gca gca gca gcc gca gcc aca tct			744
Lys Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Thr Ser			
110	115	120	
cag gac cct gag caa cac ctg act gag ctg agg gaa cca gct cct ggc			792
Gln Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly			
125	130	135	
acc aac cag cgc cag ccc agc aag aaa gcc tca aag ggc aag ggg ctc			840
Thr Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu			
140	145	150	
cga ggg agc gcc aag att tgg tcc aag tgc aat tgaaagaact gtcgtttcct			893
Arg Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn			
155	160	165	
ccctggggat gtgggggtccc agctgcctgc ctgcctctta ggagtcctca gagagccttc			953
tgtgcccctg gccagctgat aatcctaggt tcatgaccct tcacctcccc taaccccaaaa			1013
catagatcac acctttctcta gggaggagtc aaatgtaggt catgtttttg ttggtacttt			1073
ctgtttttttg tgacttcatg tgttccattg ctccccgctg ccatgctctc tcccttgttt			1133
ccttaagagc tcagcatctg tccctgttca ttacatgtca ttgagtaggt gggtagccct			1193
gatgggggtc gctctgtctg gagcataaacc cacaggcggt ttttctgccca ccccatccct			1253
gcatgcctga tccccagttc ctatacccta cccctgacct attgagcagc ctctgaagag			1313
ccatagggcc cccaccttta ctacacacct gagaattctg ggagccagtc tgccatgccca			1373
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ctctggccct tgggtcctgg gaatgctgct gcttcaacct cagagcctaa gaatggcagc			1493
cgtttcttaa catgttgaga gatgattctt tcttggccct ggccatctcg ggaagcttga			1553

tggcaatcct	ggaagggttt	aatctccttt	tgtgagtttg	gtggggaagg	gaaggggtata	1613
tagattatat	taaaaaaaaa	aaggtatata	tgcatatata	tatatataat	atgacgcaga	1673
aataaatcta	tgagaaatcc	aaaaaaaaaa	aa			1705

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 <212> DNA
 <213> Homo sapiens

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 <222> 135..206

<221> polyA_signal
 <222> 850..855

<221> polyA_site
 <222> 1056..1069

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agtgaggaaag	ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act					170
	Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr					
	1 5 10					
acc tac aac aag cac att aac atc agc ttc cac agg taacctgggc						216
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg						
	15 20					
agggagtggt	ggtgacggaa	actggagttc	ctattgtggc	tatcgcttgt	gtggaaggaa	276
caggaggatt	ctgctaattc	taataacttt	cccagctggt	agcaggggaag	catcgatatgt	336
cccttctgtgt	tctcaaatct	gcccattgt	tctctgcttt	cggggaagct	ttactcattt	396
tctaaaaagaa	atccaagtac	tgtttggtca	ttacccttta	gtaaaaaaaa	gtaacaggag	456
gatatacgtaa	tttttactgt	ttttattcct	ctgttagacc	gggccttgac	atgaatgacg	516
ccgtaaggga	gaaagagatc	ttcccaatca	gcaatcaccg	taaaagcctg	ctgtgttccc	576
gttaaaaatta	ggaaattctc	actagatgaa	ttgacatggg	aggcatttag	atttctaata	636
gtcacatagt	aattctgcgg	aggaattgag	tcattcttga	tagccatgga	attaagcgat	696
gttaattaaa	gtgcaaacga	taacctttct	gttcttacta	gaatagagta	ataaaaagaa	756
cctaggtttt	cttttgtttg	ctggaagaaa	aatcaaaatt	cttttagttct	gtcaaaccag	816
aactcttgaa	agcactttga	acaatgcctg	gaaaataaca	ggtactctgt	aaatgtttac	876
cttctctgca	agtgccctgcc	acgtgcccga	agaaaagaca	cattaaaaag	ttaagtgaca	936
ccagtcctga	ttttatataat	tttatatacc	taacaacgta	tatgttagta	tgtagaaatt	996
atatacctga	cctttttccc	tacctattac	gaactgtact	tttattaaaa	gctgccacta	1056
aaaaaaaaaa	aaa					1069

<210> 59
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 <212> DNA
 <213> Homo sapiens

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<221> polyA_signal
<222> 909..914

<221> polyA_site
<222> 1071..1084

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cctctgccag aagaaagctt agcagccagc gcctcagtag aggcctaagg gcgctgaatg 120
agtgggaaag ggaa atg ccg acc aat tgc gct gcg gcg ggc tgt gcc act 170
Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr
1 5 10
acc tac aac aag cac att aac atc agc ttc cac agg ttt cct ttg gat 218
Thr Tyr Asn Lys His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp
15 20 25
cct aaa aga aga aaa gaa tgg gtt cgc ctg gtt agg cgc aaa aat ttt 266
Pro Lys Arg Arg Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe
30 35 40
gtg cca gga aaa cac act ttt ctt tgt tca aag cac ttt gaa gcc tcc 314
Val Pro Gly Lys His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser
45 50 55 60
tgt ttt gac cta aca gga caa act cga cga ctt aaa atg gat gct gtt 362
Cys Phe Asp Leu Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val
65 70 75
cca acc att ttt gat ttt tgt acc cat ata aag tct atg aaa ctc aag 410
Pro Thr Ile Phe Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys
80 85 90
tca agg aat ctt ttg aag aaa aac aac agt tgt tct cca gct gga cca 458
Ser Arg Asn Leu Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro
95 100 105
tct agt tta aaa tca aac att agt agt cag caa gta cta ctt gaa cac 506
Ser Ser Leu Lys Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His
110 115 120
agc tat gcc ttt agg aat cct atg gag gca aaa aag agg atc att aaa 554
Ser Tyr Ala Phe Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys
125 130 135 140
ctg gaa aaa gaa ata gca agc tta aga aga aaa atg aaa act tgc cta 602
Leu Glu Lys Glu Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu
145 150 155
caa aag gaa cgc aga gca act cga aga tgg atc aaa gcc atg tgt ttg 650
Gln Lys Glu Arg Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu
160 165 170
gta aag aat tta gaa gca aat agt gta tta cct aaa ggt aca tca gaa 698
Val Lys Asn Leu Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu
175 180 185
cac atg tta cca act gcc tta agc agt ctt cct ttg gaa gat ttt aag 746
His Met Leu Pro Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys
190 195 200
atc ctt gaa caa gat caa caa gat aaa aca ctg cta agt cta aat cta 794
Ile Leu Glu Gln Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu
205 210 215 220
aaa cag acc aag agt acc ttc att taaatttagc ttgcacagag cttgatgcct 848
Lys Gln Thr Lys Ser Thr Phe Ile
225
atccttcatt cttttcagaa gtaaagataa ttatggcact tatgcaaaaa ttcattattt 908
aataaagttt tacttgaagt aacattactg aatttggtgaa gacttgatta caaaagaata 968
aaaaacttca tatggaaatt ttatttgaaa atgagtgga ggcgcttaca ttagaattac 1028

ggacttaaaaa attttgctaa taaattgtgt gtttgaaagg tgaaaaaaaa aaaaaa

1084

<210> 60
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<212> DNA
<213> Homo sapiens

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<222> 33..290

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<222> 33..92
<223> Von Heijne matrix
score 5.4
seq WFWHSSALGLVLA/PP

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Met Asn Leu His Phe Pro Gln
-20 -15
tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca cct ttc 101
Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro Pro Phe
-10 -5 1
tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt agg cta 149
Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys Arg Leu
5 10 15
tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc tgt tta 197
Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr Cys Leu
20 25 30 35
tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa aat tgt 245
Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys Asn Cys
40 45 50
aat agt cgg cac gct gga ttt gta ggg cca gca aaa ttg cgg cag 290
Asn Ser Arg His Ala Gly Phe Val Gly Pro Ala Lys Leu Arg Gln
55 60 65
tgaaactagt ttcacttcta aagcccttca tttcccacaa ggttaagctc tcgaaacccc 350
atttgatcct tggttcctat ttcgatcctc ctttggaaac tgaaaatcgg tctccatgtt 410
gtatgcaaa 419

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<212> DNA
<213> Homo sapiens

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<222> 485..616

<221> polyA_site
<222> 669..682

<400> 61

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tattttattg atcacatctt taatcttttg ttctctatac gtggcctgtt ttgatttatt    180
ttactattct tgctttctaa ggtaagtatt ttgttggtga gtgctttatt tttttcatct    240
ttcttcttga ataataatga catttttagg ttataaattt tcctctggta ctcagtttgc    300
ctcattaatt ttggcagtaa gcattctcct tttattgctt tctatgtagt ctttaatttt    360
gcttttaact tcttctttga tctaaggatt acctacttgt taatttccaa atattatctt    420
atctatctat ctatctatct atctatctat ctatctatct acctatgtga gacgaagtct    480
ggct atg tcg ccg agg ctg gag tgc agt ggt gca atc ttg gct cac tgc    529
    Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys
      1             5             10             15
aac ccc cgc ctc cca ggt tca agt tat tct cct gcc tca gct act tgg    577
Asn Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp
      20             25             30
gtg aga gga tcc ctt gag ccg ggg agg ttg agg ctg cag tgagccataa    626
Val Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
      35             40
ccactactct ccagcctgga taacaaaagt gagactctga ccaaaaaaaaa aaaaaa    682

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<213> Homo sapiens
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<221> CDS
<222> 54..995
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<222> 54..227
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<222> 1130..1135
<221> polyA_site
<222> 1181..1191

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                               Met
cag aat gtg att aat act gtg aag gga aag gca ctg gaa gtg gct gag    104
Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala Glu
      -55             -50             -45
tac ctg acc ccg gtc ctc aag gaa tca aag ttt agg gaa aca ggt gta    152
Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly Val
      -40             -35             -30
att acc cca gaa gag ttt gtg gca gct gga gat cac cta gtc cac cac    200
Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His His
      -25             -20             -15             -10
tgt cca aca tgg caa tgg gct aca ggg gaa gaa ttg aaa gtg aag gca    248
Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys Ala
      -5             1             5

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tac cta cca aca ggc aaa caa ttt ttg gta acc aaa aat gtg ccg tgc	296
Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro Cys	
10 15 20	
tat aag cgg tgc aaa cag atg gaa tat tca gat gaa ttg gaa gct atc	344
Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp Glu Leu Glu Ala Ile	
25 30 35	
att gaa gaa gat gat ggt gat ggc gga tgg gta gat aca tat cac aac	392
Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val Asp Thr Tyr His Asn	
40 45 50 55	
aca ggt att aca gga ata acg gaa gcc gtt aaa gag atc aca ctg gaa	440
Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys Glu Ile Thr Leu Glu	
60 65 70	
aat aag gac aat ata agg ctt caa gat tgc tca gca cta tgt gaa gag	488
Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser Ala Leu Cys Glu Glu	
75 80 85	
gaa gaa gat gaa gat gaa gga gaa gct gca gat atg gaa gaa tat gaa	536
Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp Met Glu Glu Tyr Glu	
90 95 100	
gag agt gga ttg ttg gaa aca gat gag gct acc cta gat aca agg aaa	584
Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr Leu Asp Thr Arg Lys	
105 110 115	
ata gta gaa gct tgt aaa gcc aaa act gat gct ggc ggt gaa gat gct	632
Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala Gly Gly Glu Asp Ala	
120 125 130 135	
att ttg caa acc aga act tat gac ctt tac atc act tat gat aaa tat	680
Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile Thr Tyr Asp Lys Tyr	
140 145 150	
tac cag act cca cga tta tgg ttg ttt ggc tat gat gag caa cgg cag	728
Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr Asp Glu Gln Arg Gln	
155 160 165	
cct tta aca gtt gag cac atg tat gaa gac atc agt cag gat cat gtg	776
Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His Val	
170 175 180	
aag aaa aca gtg acc att gaa aat cat cct cat ctg cca cca cct ccc	824
Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro Pro	
185 190 195	
atg tgt tca gtt cac cca tgc agg cat gct gag gtg atg aag aaa atc	872
Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys Ile	
200 205 210 215	
att gag act gtt gca gaa gga ggg gga gaa ctt gga gtt cat atg tat	920
Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu Gly Val His Met Tyr	
220 225 230	
ctt ctt att ttc ttg aaa ttt gta caa gct gtc att cca aca ata gaa	968
Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile Glu	
235 240 245	
tat gac tac aca aga cac ttc aca atg taatgaagag agcataaaat	1015
Tyr Asp Tyr Thr Arg His Phe Thr Met	
250 255	
ctatcctaatt tattggttct gatttttaaa gaattaaccc atagatgtga ccattgacca	1075
tattcatcaa tatatacagt ttctctaata agggacttat atgtttatgc attaaataaa	1135
aatatgttcc actaccagcc ttacttgttt aataaaaaatc agtgcaaaaa aaaaaa	1191

<210> 63

<211> 1008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 657..923

<221> sig_peptide

<222> 657..896

<223> Von Heijne matrix

score 3.5

seq RGLLSACAPWGDG/ST

<221> polyA_signal

<222> 957..962

<221> polyA_site

<222> 974..1008

<400> 63

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ntcgnatgtg gcacaaaacc cctctgctgg ctcattgtgt caactgagac tgtcagagca      60
tggctagctc tgggggtccag ctctgctggg tgggggctag agaggaagca gggagtatct      120
gcacacagga tgcctgcgct cagggtggtg cagaagtcag tgcccaggcc ccccccacaca      180
gtcccccagg gtccggcctc cccagcgagg ggctcctcgt ttgaggggag gtgacttccc      240
tcccagcagg ctcttggaac cagtaagctt cccagccctt gcctgagcag cctttcctcc      300
ttgcccgtgt ccccccctcc cggtccagtc ccaggagctt cccagggaag tggtcgaccc      360
ctccagtggc tggggcactc tgctagagtc catccgcca gctgggggca tcggcaaggc      420
caagctgcgc agcatgaagg agcgaaagct ggagaagaag aagcagaagg agcaggagca      480
agtgagagcc acgagccaag gtgggcactt gatgtcggat ctcttcaaca agctgggcat      540
gaggcgcaag ggcattctct ggaaagaacc tggggctggt gaggggcccg gaggagcctt      600
tgcccgctgt tcagactcca tccctcctct gccgccaccg cagcagccac aggtag atg      659
Met
-80
agg aca agg acg act ggg aat cct agg ggg ctc cat gac acc ttc ccc      707
Arg Thr Arg Thr Thr Gly Asn Pro Arg Gly Leu His Asp Thr Phe Pro
-75 -70 -65
cgc aga ccc aga ctt ggc cgt tgc tct gac atg gac aca gcc agg aca      755
Arg Arg Pro Arg Leu Gly Arg Cys Ser Asp Met Asp Thr Ala Arg Thr
-60 -55 -50
agc tgc tca gac ctg ctt ccc tgg gag ggg gtg acg gaa cca gca ctg      803
Ser Cys Ser Asp Leu Leu Pro Trp Glu Gly Val Thr Glu Pro Ala Leu
-45 -40 -35
tgt gga gac cag ctt caa gga acg gaa ggc tgg ctt gag gcc aca cag      851
Cys Gly Asp Gln Leu Gln Gly Thr Glu Gly Trp Leu Glu Ala Thr Gln
-30 -25 -20
ctg ggg cgg gga ctt ctg tct gcc tgt gct cca tgg ggg gac ggc tcc      899
Leu Gly Arg Gly Leu Leu Ser Ala Cys Ala Pro Trp Gly Asp Gly Ser
-15 -10 -5 1
acc cag cct gtg cca ctg tgt tct taagaggctt ccagagaaaa cggcacacca      953
Thr Gln Pro Val Pro Leu Cys Ser
5
atcaataaag aactgagcag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaan      1008
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<210> 64

<211> 568

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 18..311

<221> sig_peptide

<222> 18..62

<223> Von Heijne matrix

score 8.4

seq AMWLLCVALAVLA/WG

<400> 64

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agtgtgtgtt acccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg      50
                Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu
                -15                -10                -5
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga      98
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg
                1                5                10
atg aag agt cgg gag cag gga gga cgg ctg gga gcc gaa agc cgg acc      146
Met Lys Ser Arg Glu Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr
                15                20                25
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc      194
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro
                30                35                40
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc      242
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys
                45                50                55                60
ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa ggt ctt      290
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu
                65                70                75
acc tct gaa ccc ctc aca gcc tagggacagg agcggccggc ttacctggtg      341
Thr Ser Glu Pro Leu Thr Ala
                80
ggttggggga cgtcggcagc tcgctgacta cgccagcagg attgaggagc agagaaacag      401
ttgcagttgg ttgtattcag tacctgcatt tccgttggga actccacctg tacttggtat      461
tctgtggaac tttttttatt tgtagaagga gcaagaatat tgaccttact atatagcaca      521
cgaaacaatc tatgctgtat cgtgcctgct caatccttaa agttaac      568

```

<210> 65

<211> 538

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 151..426

<221> sig_peptide

<222> 151..258

<223> Von Heijne matrix

score 5.2

seq KVALAGLLGFGLG/KV

<221> polyA_signal

<222> 505..510

<221> polyA_site

<222> 527..538

<400> 65

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cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcac      60
catggcttca gcgtctgctc gtggaaacca agataaagat gcccatTTTtc caccaccaag      120
caagcagctc tgcctTTTTc tcttgtaagc atg ctt gtc acc cag gga cta gtc      174
                               Met Leu Val Thr Gln Gly Leu Val
                               -35                               -30
tac caa ggt tat ttg gca gct aat tct aga ttt gga tca ttg ccc aaa      222
Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys
                               -25                               -20                               -15
gtt gca ctt gct ggt ctc ttg gga ttt ggc ctt gga aag gta tca tac      270
Val Ala Leu Ala Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr
                               -10                               -5                               1
ata gga gta tgc cag agt aaa ttc cat ttt ttt gaa gat cag ctc cgt      318
Ile Gly Val Cys Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg
5                               10                               15                               20
ggg gct ggt ttt ggt cca cag cat aac agg cac tgc ctc ctt acc tgt      366
Gly Ala Gly Phe Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys
                               25                               30                               35
gag gaa tgc aaa ata aag cat gga tta agt gag aag gga gac tct cag      414
Glu Glu Cys Lys Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln
                               40                               45                               50
cct tca gct tcc taaattctgt gtctgtgact ttcgaagttt tttaaacctc      466
Pro Ser Ala Ser
                               55
Tgaatttgta cacatttaaaa atttcaagtg tacttttaaaa taaaatactt ctaatggaac      526
aaaaaaaaaa aa      538

```

<210> 66

<211> 1747

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 10..1062

<221> sig_peptide

<222> 10..57

<223> Von Heijne matrix

score 4.9

seq FIYLAQHFTLCSG/WS

<221> polyA_signal

<222> 1710..1715

<221> polyA_site

<222> 1735..1747

<400> 66

```

gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt      51

```

Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys															
-15				-10				-5							
tct	ggg	tgg	tcc	agc	aca	tac	cgg	gac	ctc	cgg	aag	ggt	gtg	tat	gtg
Ser	Gly	Trp	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val
1				5				10							
ccc	tac	acc	cag	ggc	aag	tgg	gaa	ggg	gag	ctg	ggc	acc	gac	ctg	gta
Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val
15				20				25				30			
agc	atc	ccc	cat	ggc	ccc	aac	gtc	act	gtg	cgt	gcc	aac	att	gct	gcc
Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala
35				40				45							
atc	act	gaa	tca	gac	aag	ttc	ttc	atc	aac	ggc	tcc	aac	tgg	gaa	ggc
Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly
50				55				60							
atc	ctg	ggg	ctg	gcc	tat	gct	gag	att	gcc	agg	cct	gac	gac	tcc	ccg
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Pro
65				70				75							
gag	cct	ttc	ttt	gac	tct	ctg	gta	aag	cag	acc	cac	gtt	ccc	aac	ctc
Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu
80				85				90							
ttc	tcc	ctg	cag	ctt	tgt	ggt	gct	ggc	ttc	ccc	ctc	aac	cag	tct	gaa
Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu
95				100				105				110			
gtg	ctg	gcc	tct	gtc	gga	ggg	agc	atg	atc	att	gga	ggt	atc	gac	cac
Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His
115				120				125							
tcg	ctg	tac	aca	ggc	agt	ctc	tgg	tat	aca	ccc	atc	cgg	cgg	gag	tgg
Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp
130				135				140							
tat	tat	gag	gtg	atc	att	gtg	cgg	gtg	gag	atc	aat	gga	cag	gat	ctg
Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu
145				150				155							
aaa	atg	gac	tgc	aag	gag	tac	aac	tat	gac	aag	agc	att	gtg	gac	agt
Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser
160				165				170							
ggc	acc	acc	aac	ctt	cgt	ttg	ccc	aag	aaa	gtg	ttt	gaa	gct	gca	gtc
Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val
175				180				185				190			
aaa	tcc	atc	aag	gca	gcc	tcc	tcc	acg	gag	aag	ttc	cct	gac	ggt	ttc
Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe
195				200				205							
tgg	cta	gga	gag	cag	ctg	gtg	tgc	tgg	caa	gca	ggc	acc	acc	cct	tgg
Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp
210				215				220							
aac	att	ttc	cca	gtc	atc	tca	ctc	tac	cta	atg	ggt	gag	gtt	acc	aac
Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn
225				230				235							
cag	tcc	ttc	cgc	atc	acc	atc	ctt	ccg	cag	caa	tac	ctg	cgg	cca	gtg
Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val
240				245				250							
gaa	gat	gtg	gcc	acg	tcc	caa	gac	gac	tgt	tac	aag	ttt	gcc	atc	tca
Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser
255				260				265				270			
cag	tca	tcc	acg	ggc	act	gtt	atg	gga	gct	gtt	atc	atg	gag	ggc	ttc
Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe
275				280				285							
tac	gtt	gtc	ttt	gat	cgg	gcc	cga	aaa	cga	att	ggc	ttt	gct	gtc	agc
290				295				300							

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Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
      290                      295                      300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc ccn      1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
      305                      310                      315
ttt tgt cac ctt gga cat gga aga ctg tgg cta caa cat tcc aca gac      1059
Phe Cys His Leu Gly His Gly Arg Leu Trp Leu Gln His Ser Thr Asp
      320                      325                      330
aga tgagtcaacc ctcacatgacca tagcctatgt catggctgcc atctgcgccc      1112
Arg
335
tcttcatgct gccactctgc ctcacatggtgt gtcagtggcg ctgcctccgc tgcctgcgcc      1172
agcagcatga tgacttttgc gatgacatct ccctgctgaa gtgaggaggc ccatgggcag      1232
aagatagga ttcccttgcg ccacacctcc gtggttccact ttggtcacia gtaggagaca      1292
cagatggcac ctgtggccag agcacctcag gaccctcccc acccaccaa tgcctctgcc      1352
ttgatggaga aggaaaaggc tggcaagggtg ggttccaggg actgtacctg taggagacag      1412
aaaagagaag aaagaagcac tctgctggcg ggaatactct tggtcacctc aaatttaagt      1472
cgggaaattc tgctgcttga aacttcagcc ctgaaccttt gtcaccattc ctttaaattc      1532
tccaacccaa agtattcttc ttttcttagt ttcagaagta ctggcatcac acgcaggtta      1592
ccttggcgty tgtccctgtg gtaccctggc agagaagaga ccaagcttgt ttccctgctg      1652
gccaagtca gtaggagagg atgcacagtt tgctatttgc tttagagaca gggactgtat      1712
aaacaagcct aacattggtg caaaaaaaaa aaaaaa      1747

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<210> 67
<211> 1686
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 78..491
<221> sig_peptide
<222> 78..218
<223> Von Heijne matrix
      score 5.8
      seq LMCFGALIGLCAC/IC

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<221> polyA_signal
<222> 1652..1657

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<221> polyA_site
<222> 1673..1686

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<400> 67
ggtatagccc accagaaagg acagagtcac ttgatgtggt cacaaaatgt gtgagtttca      60
cactaactga gcagttc atg gag aaa ttt gtt gat ccc gga aac cac aat      110
      Met Glu Lys Phe Val Asp Pro Gly Asn His Asn
      -45                      -40
agc ggg att gat ctc ctt agg acc tat ctt tgg cgt tgc cag ttc ctt      158
Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu
      -35                      -30                      -25
tta cct ttt gtg agt tta ggt ttg atg tgc ttt ggg gct ttg atc gga      206
Leu Pro Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly
      -20                      -15                      -10                      -5

```

ctt tgt gct tgc att tgc cga agc tta tat ccc acc att gcc acg ggc	254
Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly	
1 5 10	
att ctc cat ctc ctt gca ggt ctg tgt aca ctg ggc tca gta agt tgt	302
Ile Leu His Leu Leu Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys	
15 20 25	
tat gtt gct gga att gaa cta ctc cac cag aaa cta gag ctc cct gac	350
Tyr Val Ala Gly Ile Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp	
30 35 40	
aat gta tcc ggt gaa ttt gga tgg tcc ttc tgc ctt gct tgt gtc tct	398
Asn Val Ser Gly Glu Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser	
45 50 55 60	
gct ccc tta cag ttc atg gct tct gct ctc ttc atc tgg gct gct cac	446
Ala Pro Leu Gln Phe Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His	
65 70 75	
acc aac cgg aga gag tac acc tta atg aag gca tat cgt gtg gca	491
Thr Asn Arg Arg Glu Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala	
80 85 90	
tgagcaagaa actgcctgct ttacaattgc cattttttatt tttttaaaat aatactgata	551
ttttcccccac ctctcaattg tttttaattt ttatttgtgg atataccatt ttattatgaa	611
aatctatttt atttatacac attcaccact aaatacacac ttaataccac taaaatttat	671
gtggtttact ttaagcgatg ccatctttca aataaaactaa tctaggtcta gacagaaaga	731
aatggataga gacttgacac aaattttatga aagaaaattg ggagtaggaa tgtgaccgaa	791
aaacaagttgt gctaattgtct gttagacttt tcagtaaaac caaagtaact gtatctgttc	851
aaactaaaaac tctatattag tttctttggg aaacctctca tcgtcaaaac tttatgttca	911
ctttgctggt gtagatagcc agtcaaccag cagtattagt gctgttttca aagatttaag	971
ctctataaaa ttgggaaatt atctaagatc attttcccta agcattgaca catagcttca	1031
tctgaggtga gatatggcag ctgtttgtat ctgcactgtg tctgtctaca aagagtga	1091
aatacagttg ttacttgaaa ttttaacttt gtaactgcaa gaattccagt tcggccgggc	1151
gaggattagt attattttta actctccgta agattttcag taccaccaa ttgttttgga	1211
ttttttttct ttcctcttca cataccaggg ttattaaaag tgtgctttct ttttacatta	1271
tattacagtt acaaggtaaa attcctcaac tgctatttat ttattccagc ccagtactat	1331
aaagaacggt tcaccataat gacctccag agctgggaaa cctaccacaa gatctaaagt	1391
actggtgtgc cattaacctc caactatggt ctttatttct tgtggttaata tgatgtgcct	1451
ttccttgctc aaatcccttc ctggtgtgta tcaacattat ttaatgtctt ctaattcagt	1511
catttttttat aagtatgtct ataaacattg aactttaaaa aacttattta tttattccac	1571
tactgtagca attgacagat taaaaaaatg taacttcata atttcttacc ataacctcaa	1631
gtgtctttttt aaaaaataaa attaaaaatg aaaagagacc caaaaaaaaa aaaaa	1686

<210> 68

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..371

<221> sig_peptide

<222> 69..287

<223> Von Heijne matrix

score 4

seq AVGFLFWIVLTS/WI

<221> polyA_signal

<222> 510..515

<221> polyA_site

<222> 530..542

<400> 68

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tgttacttag ggtcaaggct tgggtcttgc cccgcaaacc cttgggacga cccggcccca    60
gcgcagct atg aac ctg gag cga gtg tcc aat gag gag aaa ttg aac ctg    110
      Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu
            -70                -65                -60

tgc cgg aag tac tac ctg ggg ggg ttt gct ttc ttg cct ttt ctc tgg    158
Cys Arg Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp
            -55                -50                -45

ttg gtc aac atc ttc tgg ttc tac cga gag gcc ttc ctt gtc cca gcc    206
Leu Val Asn Ile Phe Trp Phe Tyr Arg Glu Ala Phe Leu Val Pro Ala
            -40                -35                -30

tac aca gaa cag agc caa atc aaa ggc tat gtc tgg cgc tca gct gtg    254
Tyr Thr Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val
            -25                -20                -15

ggc ttc ctc ttc tgg gtg ata gtg ctc acc tcc tgg atc acc atc ttc    302
Gly Phe Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe
            -10                -5                1                5

cag atc tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc    350
Gln Ile Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe
            10                15                20

acc ata ccc ctg ggc acc ccc tgacaacttc tgcacatact ggggcctgc    401
Thr Ile Pro Leu Gly Thr Pro
            25

ttattctccc aggacaggct ccttaaagca gaggagcctg tcctgggagc cccttctcaa    461
actcctaaga cttgttctca tgtcccacgt tctctgctga catcccccaa taaaggaccc    521
taactttcaa aaaaaaaaaa a    542

```

<210> 69

<211> 1174

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..757

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_site

<222> 1160..1174

<400> 69

```

g atg cct gag ggc ccc gag ctg cac ctg gcc agc cag ttt gtg aat gag    49
      Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
            -65                -60                -55

gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc    97

```

Ala	Cys	Arg	Ala	Leu	Val	Phe	Gly	Gly	Cys	Val	Glu	Lys	Ser	Ser	Val	
		-50					-45					-40				
agc	cgc	aac	cct	gag	gtg	ccc	ttt	gag	agc	agt	gcc	tac	cgc	atc	tca	145
Ser	Arg	Asn	Pro	Glu	Val	Pro	Phe	Glu	Ser	Ser	Ala	Tyr	Arg	Ile	Ser	
		-35					-30					-25				
gct	tca	gcc	cgc	ggc	aag	gag	ctg	cgc	ctg	ata	ctg	agc	cct	ctg	cct	193
Ala	Ser	Ala	Arg	Gly	Lys	Glu	Leu	Arg	Leu	Ile	Leu	Ser	Pro	Leu	Pro	
		-20					-15				-10				-5	
ggg	gcc	cag	cct	caa	cag	gag	cca	ctg	gcc	ctg	gtc	ttc	cgc	ttc	ggc	241
Gly	Ala	Gln	Pro	Gln	Gln	Glu	Pro	Leu	Ala	Leu	Val	Phe	Arg	Phe	Gly	
			1				5					10				
atg	tcc	ggc	tct	ttt	cag	ctg	gtg	ccc	cgc	gag	gag	ctg	cca	cgc	cat	289
Met	Ser	Gly	Ser	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His	
		15					20					25				
gcc	cac	ctg	cgc	ttt	tac	acg	gcc	ccg	cct	ggc	ccc	cgg	ctc	gcc	cta	337
Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu	
		30					35					40				
tgt	ttc	gtg	gac	atc	cgc	cgg	ttc	ggc	cgc	tgg	gac	ctt	ggg	gga	aag	385
Cys	Phe	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys	
					50					55					60	
tgg	cag	ccg	ggc	cgc	ggg	ccc	tgt	gtc	ttg	cag	gag	tac	cag	cag	ttc	433
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe	
				65					70					75		
agg	gag	aat	gtg	cta	cga	aac	cta	gcg	gat	aag	gcc	ttt	gac	cgg	ccc	481
Arg	Glu	Asn	Val	Leu	Arg	Asn	Leu	Ala	Asp	Lys	Ala	Phe	Asp	Arg	Pro	
		80							85				90			
atc	tgc	gag	gcc	ctc	ctg	gac	cag	agg	ttc	ttc	aat	ggc	att	ggc	aac	529
Ile	Cys	Glu	Ala	Leu	Leu	Asp	Gln	Arg	Phe	Phe	Asn	Gly	Ile	Gly	Asn	
		95					100					105				
cat	ctg	cgg	gca	gag	atc	ctg	tac	cgg	ctg	aag	atc	ccc	ccc	ttt	gag	577
Tyr	Leu	Arg	Ala	Glu	Ile	Leu	Tyr	Arg	Leu	Lys	Ile	Pro	Pro	Phe	Glu	
		110					115					120				
aag	gcc	cgc	tcg	gtc	ctg	gag	gcc	ctg	cag	cag	cac	agg	ccg	agc	ccg	625
Lys	Ala	Arg	Ser	Val	Leu	Glu	Ala	Leu	Gln	Gln	His	Arg	Pro	Ser	Pro	
		125				130						135			140	
gag	ctg	acc	ctg	agc	cag	aag	ata	agg	acc	aag	ctg	cag	aat	tca	gac	673
Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile	Arg	Thr	Lys	Leu	Gln	Asn	Ser	Asp	
				145					150				155			
ctg	ctg	gag	cta	tgt	cac	tca	gtg	ccc	aag	gaa	gtg	gtc	cag	ttg	ggc	721
Leu	Leu	Glu	Leu	Cys	His	Ser	Val	Pro	Lys	Glu	Val	Val	Gln	Leu	Gly	
			160						165				170			
gag	gcc	aaa	gat	ggc	agc	aac	ctc	tgc	ttc	agc	aaa	tgattgtgta				767
Glu	Ala	Lys	Asp	Gly	Ser	Asn	Leu	Cys	Phe	Ser	Lys					
		175					180									
accctggggc	acttggtccc	ctctggac	ct	gattcaccga	tttggaa	gatt	gtagcccta									827
gctgatactc	aatggactag	gcctcctcac	ttgtcaatag	tggttccagg	ctgggcgcag											887
tggctcatgc	ctgtgggtccc	ggcacttcgg	gaggccgagt	ggggtggctc	acctgaggtc											947
aggagttcga	gaccatcctg	gccaacatgg	tgaaacccca	tctccactaa	aatgcaaaaa											1007
attagccagg	tggtggtggcg	ggcacctgta	gtctcagcta	ctcgggagga	tgaggcagga											1067
aaatcgcttg	aacccaggag	gtggaggttg	cagttgagct	gagatcgtgc	cattgcactc											1127
cagcctgggc	aacgagagca	aaactccatc	tcaaaaaaaa	aaaaaaa												1174

<210> 70

<211> 1285

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..1051

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_signal

<222> 1248..1253

<221> polyA_site

<222> 1272..1285

<400> 70

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Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu

-65

-60

-55

gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc 97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val

-50

-45

-40

agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca 145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser

-35

-30

-25

gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct 193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro

-20

-15

-10

-5

ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc 241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly

1

5

10

atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat 289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His

15

20

25

gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta 337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu

30

35

40

tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag 385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys

45

50

55

60

tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc 433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe

65

70

75

agg ctg aag atc ccc ccc ttt gag aag gcc cgc tcg gtc ctg gag gcc 481
Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala

80

85

90

ctg cag cag cac agg ccg agc ccg gag ctg acc ctg agc cag aag ata 529
Leu Gln Gln His Arg Pro Ser Pro Glu Leu Thr Leu Ser Gln Lys Ile

95

100

105

agg acc aag ctg cag aat cca gac ctg ctg gag cta tgt cac tca gtg 577
Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu Glu Leu Cys His Ser Val

110

115

120

ccc aag gaa gtg gac cag ttg ggg ggc agg ggc tac ggg tca gag agc 625
Pro Lys Glu Val Asp Gln Leu Gly Gly Arg Gly Tyr Gly Ser Glu Ser

125	130	135	140	
ggg gag gag gac ttt gct gcc ttt cga gcc tgg ctg cgc tgc tat ggc				673
Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala Trp Leu Arg Cys Tyr Gly				
145	150	155		
atg cca ggc atg agc tcc ctg cag gac cgg cat ggc cgt acc atc tgg				721
Met Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp				
160	165	170		
ttc cag ggc gat cct gga ccg ttg gca ccc aaa ggc cgc aag tcc cgc				769
Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro Lys Gly Arg Lys Ser Arg				
175	180	185		
aaa aag aaa tcc aag gcc aca cag ctg agt cct gag gac aga gtg gag				817
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu				
190	195	200		
gac gct ttg cct cca agc aag gcc cct tcc aag aca cga agg gca aag				865
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Lys Thr Arg Arg Ala Lys				
205	210	215	220	
aga gac ctt cct aag agg act gca acc cag cgg cct gag ggg acc agc				913
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser				
225	230	235		
ctc cag cag gac cca gaa gct ccc aca gtg ccc aag aag ggg agg agg				961
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg				
240	245	250		
aag ggc cga cag gca gcc tct ggc cac tgc aga ccc cgg aag gtc aag				1009
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys				
255	260	265		
gct gac atc cca tcc ttg gaa cca gag ggg acc tca gcc tct				1051
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser				
270	275	280		
tagcaggagg ctctccttgc ttgcactcac cctttcttat tgtcttgccc tgcattctggg				1111
ggctctgaatt tttgggagca ggcaatatct gaaggtgcaa acaggcccta cggctgttcc				1171
ctgcacaact ctcattggtt taattgtacc ccattctcca catctttaa gctcatgtga				1231
aaaatgctgc atttttaata aactgatata tttgaactcc aaaaaaaaaa aaaa				1285

<210> 71

<211> 1398

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..1171

<221> sig_peptide

<222> 2..205

<223> Von Heijne matrix

score 7.3

seq LRLILSPLPGAQP/QQ

<221> polyA_signal

<222> 1368..1373

<221> polyA_site

<222> 1386..1398

<400> 71

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Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu	
-65 -60 -55	
gcc tgc agg gcg ctg gtg ttc ggc ggc tgc gtg gag aag tcc tct gtc	97
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val	
-50 -45 -40	
agc cgc aac cct gag gtg ccc ttt gag agc agt gcc tac cgc atc tca	145
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser	
-35 -30 -25	
gct tca gcc cgc ggc aag gag ctg cgc ctg ata ctg agc cct ctg cct	193
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro	
-20 -15 -10 -5	
ggg gcc cag ccc caa cag gag cca ctg gcc ctg gtc ttc cgc ttc ggc	241
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly	
1 5 10	
atg tcc ggc tct ttt cag ctg gtg ccc cgc gag gag ctg cca cgc cat	289
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His	
15 20 25	
gcc cac ctg cgc ttt tac acg gcc ccg cct ggc ccc cgg ctc gcc cta	337
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu	
30 35 40	
tgt ttc gtg gac atc cgc cgg ttc ggc cgc tgg gac ctt ggg gga aag	385
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys	
45 50 55 60	
tgg cag ccg ggc cgc ggg ccc tgt gtc ttg cag gag tac cag cag ttc	433
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe	
65 70 75	
agg gag aat gtg cta cga aac cta gcg gat aag gcc ttt gac cgg ccc	481
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro	
80 85 90	
atc tgc gag gcc ctc ctg gac cag agg ttc ttc aat ggc att ggc aac	529
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn	
95 100 105	
tat ctg cgg gca gag atc ctg tac cgg ctg aag atc ccc ccc ttt gag	577
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu	
110 115 120	
aag gcc cgc tcg gtc ctg gag gcc ctg cag cag cac agg ccg agc ccg	625
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro	
125 130 135 140	
gag ctg acc ctg agc cag aag ata agg acc aag ctg cag aat cca gac	673
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp	
145 150 155	
ctg ctg gag cta tgt cac tca gtg ccc aag gaa gtg gtc cag ttg ggg	721
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly	
160 165 170	
ggc aga ggc tac ggg tca gag agc ggg gag gag gac ttt gct gcc ttt	769
Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe	
175 180 185	
cga gcc tgg ctg cgc tgc tat ggc atg cca ggc atg agc tcc ctg cag	817
Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln	
190 195 200	
gac cgg cat ggc cgt acc atc tgg ttc cag ggg gat cct gga ccg ttg	865
Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu	
205 210 215 220	
gca ccc aaa ggg cgc aag tcc cgc aaa aag aaa tcc aag gcc aca cag	913
Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln	
225 230 235	

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ctg agt cct gag gac aga gtg gag gac gct ttg cct ccg agc aag gcc      961
Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala
      240                      245                      250

cct tcc agg aca cga agg gca aag aga gac ctt cct aag agg act gca      1009
Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala
      255                      260                      265

acc cag cgg cct gag ggg acc agc ctc cag cag gac cca gaa gct ccc      1057
Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro
      270                      275                      280

aca gtg ccc aag aag ggg agg agg aag ggg cga cag gca gcc tct ggc      1105
Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly
      285                      290                      295                      300

cac tgc aga ccc cgg aag gtc aag gct gac atc cca tcc ttg gaa cca      1153
His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro
      305                      310                      315

gag ggg acc tca gcc tct tagcaggagg ctctccttgc ttgcactcac      1201
Glu Gly Thr Ser Ala Ser
      320

cctttcttat tgtcttgccc tgcattctggg ggtctgaatt tttgggagca ggcaatatct      1261
gaaggtgcaa acaggcccta cggctgttcc ctgcacaact ctcatggttt taattgtacc      1321
ccatcttcca catctttaaa gtcattgtga aaaatgctgc atttttaata aactgataca      1381
tttgaaaaaa aaaaaaa      1398

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<210> 72
<211> 821
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..611

<221> sig_peptide
<222> 42..287
<223> Von Heijne matrix
      score 4.4
      seq NLPHLQVVGLTWG/HI

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<221> polyA_signal
<222> 787..792

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<221> polyA_site
<222> 808..821

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<400> 72
ccgttgccag ttctgcgcgt gtcctgcgtc tccagtatgg a atg tat gtt tgg ccc      56
                                   Met Tyr Val Trp Pro
                                   -80

tgt gct gtg gtc ctg gcc cag tac ctt tgg ttt cac aga aga tct ctg      104
Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe His Arg Arg Ser Leu
      -75                      -70                      -65

cca ggc aag gcc atc tta gag att gga gca gga gtg agc ctt cca gga      152
Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly Val Ser Leu Pro Gly
      -60                      -55                      -50

att ttg act gcc aaa tgt ggt gca gaa gta ata ctg tca gac agc tca      200

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Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile Leu Ser Asp Ser Ser
-45          -40          -35          -30
gaa ctg cct cac tgt ctg gaa gtc tgt cgg caa agc tgc caa atg aat      248
Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln Ser Cys Gln Met Asn
          -25          -20          -15
aac ctg cca cat ctg cag gtg gta gga cta aca tgg ggt cat ata tct      296
Asn Leu Pro His Leu Gln Val Val Gly Leu Thr Trp Gly His Ile Ser
          -10          -5          1
tgg gat ctt ctg gct cta cca cca caa gat att atc ctt gca tct gat      344
Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile Ile Leu Ala Ser Asp
          5          10          15
gtg ttc ttt gaa cca gaa gat ttt gaa gac att ttg gct aca ata tat      392
Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile Leu Ala Thr Ile Tyr
          20          25          30          35
ttt ttg atg cac aag aat ccc aag gtc caa ttg tgg tct act tat caa      440
Phe Leu Met His Lys Asn Pro Lys Val Gln Leu Trp Ser Thr Tyr Gln
          40          45          50
gtt agg agt gct gac tgg tca ctt gaa gct tta ctc tac aaa tgg gat      488
Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu Leu Tyr Lys Trp Asp
          55          60          65
atg aaa tgt gtc cac att cct ctt gag tct ttt gat gca gac aaa gaa      536
Met Lys Cys Val His Ile Pro Leu Glu Ser Phe Asp Ala Asp Lys Glu
          70          75          80
gat ata gca gaa tct acc ctt cca gga aga cat aca gtt gaa atg ctg      584
Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His Thr Val Glu Met Leu
          85          90          95
gtc att tcc ttt gca aag gac agt ctc tgaattatac ctacaacctg      631
Val Ile Ser Phe Ala Lys Asp Ser Leu
          100          105
ttctggggaca gtatcaatac tgatgagcaa cctggcacac aaactatgag cagaccactt      691
cagcttgaga atgcagtggg tctgaagatg gtcaagtctg tctgccttag attttgatgt      751
cacctagaca acacttaaac tcatatgaaa caaaaattaa aatacgtatt acaagtaaaa      811
aaaaaaaaaa      821

<210> 73
<211> 916
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..916

<221> sig_peptide
<222> 62..757
<223> Von Heijne matrix
      score 4.2
      seq LVTPAALRPLVLG/GN

<221> polyA_site
<222> 904..916

<400> 73
cctgaatgac ttgaatgttt cccgcctga gctaacagtc catgtgggtg attcagctct      60
g atg gga tgt gtt ttc cag agc aca gaa gac aaa cgt ata ttc aag ata      109

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Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile																			
-230						-225						-220							
gac	tgg	act	ctg	tca	cca	gga	gag	cac	gcc	aag	gac	gaa	tat	gtg	cta		157		
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu				
-215						-210						-205							
tac	tat	tac	tcc	aat	ctc	agt	gtg	cct	att	ggg	cgc	ttc	cag	aac	cgc		205		
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg				
-200						-195						-190						-185	
gta	cac	ttg	atg	ggg	gac	aac	tta	tgc	aat	gat	ggc	tct	ctc	ctg	ctc		253		
Val	His	Leu	Met	Gly	Asp	Asn	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu				
-180						-175						-170							
caa	gat	gtg	caa	gag	gct	gac	cag	gga	acc	tat	atc	tgt	gaa	atc	cgc		301		
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg				
-165						-160						-155							
ctc	aaa	ggg	gag	agc	cag	gtg	ttc	aag	aag	gcg	gtg	gta	ctg	cat	gtg		349		
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val				
-150						-145						-140							
ctt	cca	gag	gag	ccc	aaa	gag	ctc	atg	gtc	cat	gtg	ggt	gga	ttg	att		397		
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu	Ile				
-135						-130						-125							
cag	atg	gga	tgt	gtt	ttc	cag	agc	aca	gaa	gtg	aaa	cac	gtg	acc	aag		445		
Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val	Thr	Lys				
-120						-115						-110						-105	
gta	gaa	tgg	ata	ttt	tca	gga	cgg	cgc	gca	aag	gag	gag	att	gta	ttt		493		
Val	Glu	Trp	Ile	Phe	Ser	Gly	Arg	Arg	Ala	Lys	Glu	Glu	Ile	Val	Phe				
-100						-95						-90							
cgt	tac	tac	cac	aaa	ctc	agg	atg	tct	gcg	gag	tac	tcc	cag	agc	tgg		541		
Arg	Tyr	Tyr	His	Lys	Leu	Arg	Met	Ser	Ala	Glu	Tyr	Ser	Gln	Ser	Trp				
-85						-80						-75							
ggc	cac	ttc	cag	aat	cgt	gtg	aac	ctg	gtg	ggg	gac	att	ttc	cgc	aat		589		
Gly	His	Phe	Gln	Asn	Arg	Val	Asn	Leu	Val	Gly	Asp	Ile	Phe	Arg	Asn				
-70						-65						-60							
gac	ggt	tcc	atc	atg	ctt	caa	gga	gtg	agg	gag	tca	gat	gga	gga	aac		637		
Asp	Gly	Ser	Ile	Met	Leu	Gln	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gly	Asn				
-55						-50						-45							
tac	acc	tgc	agt	atc	cac	cta	ggg	aac	ctg	gtg	ttc	aag	aaa	acc	att		685		
Tyr	Thr	Cys	Ser	Ile	His	Leu	Gly	Asn	Leu	Val	Phe	Lys	Lys	Thr	Ile				
-40						-35						-30						-25	
gtg	ctg	cat	gtc	agc	ccg	gaa	gag	cct	cga	aca	ctg	gtg	acc	ccg	gca		733		
Val	Leu	His	Val	Ser	Pro	Glu	Glu	Pro	Arg	Thr	Leu	Val	Thr	Pro	Ala				
-20						-15						-10							
gcc	ctg	agg	cct	ctg	gtc	ttg	ggt	ggt	aat	cag	ttg	gtg	atc	att	gtg		781		
Ala	Leu	Arg	Pro	Leu	Val	Leu	Gly	Gly	Asn	Gln	Leu	Val	Ile	Ile	Val				
-5						1						5							
gga	att	gtc	tgt	gcc	aca	atc	ctg	ctg	ctc	cct	gtc	ctg	ata	ttg	atc		829		
Gly	Ile	Val	Cys	Ala	Thr	Ile	Leu	Leu	Leu	Pro	Val	Leu	Ile	Leu	Ile				
10						15						20							
gtg	aag	aag	acc	tgt	gga	aat	aag	agt	tca	gtg	aat	tct	aca	gtc	ttg		877		
Val	Lys	Lys	Thr	Cys	Gly	Asn	Lys	Ser	Ser	Val	Asn	Ser	Thr	Val	Leu				
25						30						35						40	
gtg	aag	aac	acg	aag	aag	act	aat	cca	aaa	aaa	aaa	aaa					916		
Val	Lys	Asn	Thr	Lys	Lys	Thr	Asn	Pro	Lys	Lys	Lys	Lys							
45						50													

<211> 1153
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..520

<221> polyA_signal
 <222> 1124..1129

<221> polyA_site
 <222> 1141..1153

<400> 74
 cctgaatgac ttgaatgttt ccccgccctga gctaacagtc catgtgggtg attcagctct 60
 g atg gga tgt gtt ttc cag agc aca gta gac aaa tgt ata ttc aag ata 109
 Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile
 1 5 10 15
 gac tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta 157
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
 20 25 30
 TAC tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc 205
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
 35 40 45
 gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc 253
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
 50 55 60
 Caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc 301
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
 65 70 75 80
 ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg 349
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 85 90 95
 ctt cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att 397
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
 100 105 110
 Cag atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag 445
 Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
 115 120 125
 gta gaa tgg ata ttt tca gga cgg cgc gca aag gta aca agg agg aaa 493
 Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys
 130 135 140
 cat cac tgt gtt aga gaa ggc tct ggc tgatggtatc aggacaaagg 540
 His His Cys Val Arg Glu Gly Ser Gly
 145 150
 tagaatcagg cacatgagga ggtgttgcaa gagcctgggc tttggtgctt atcagaactg 600
 gaccttctcc tagcaatttc agctttctgg tgggaaaagg aactccaatg aagaacaaga 660
 acaagaagat gatgatgatg cttaactttt tggatgccga tatgagattg tacatgtaaa 720
 gcattttgta taagacttgg cccctgcatt ttagtttcct tctttctccc ttttcttcg 780
 tatagagtcc atgggagaaat gagggagatg atttttgtgg ccagccaag aaagcaatgg 840
 gctagacatt aaaatgatta cacttttatt ctactggggg ttagttctgt gagttttcat 900
 ctgtgccccca ttgccccatt tatgtgatgg aggggaatttt catgggtact tcacgtgttg 960
 ggattgattg atcctggggg ccagggtgaa gggatattta cgggacctct ataaagcagg 1020
 aagaagcaag tttattcttt agaccagtag ctctcaacca tgatgtggtc atatatttat 1080
 gggtaacat gtgttggtgg gatatcccaa gtaacttggt attaataaaa gttaagtgtc 1140
 aaaaaaaaaaaa aaa 1153

<210> 75
 <211> 1517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..167

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<400> 75
ctctgaaatg cttgtctttt atg ctg gna ggt gac cat agg gct ctg ctt tta      53
                Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu
                1          5          10
aag ata tgg ctg ctt caa agg cca gag tca cag gaa gga ctt ctt cca      101
Lys Ile Trp Leu Leu Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro
                15          20          25
ggg aga tta gtg gtg atg gag agg aga gtt aaa atg acc tca tgt cct      149
Gly Arg Leu Val Val Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro
                30          35          40
ctct tgt cca cgg ttt tgt tgagttttca ctcttctaata gcaagggctct      197
Ser Cys Pro Arg Phe Cys
                45
cacactgtga accacttagg atgtgatcac tttcaggtgg ccaggaatgt tgaatgtctt      257
tggtctcagtt catttaaaaa agatatctat ttgaaagtgc tcagagttgt acatatgttt      317
cacagtacag gatctgtaca taaaagtgttc tttcctaaac cattcaccaa gagccaatat      377
ctaggcattt tcttggtagc acaaattttc ttattgctta gaaaattgtc ctccttggtta      437
tttctgtttg taagacttaa gtgagttagg tctttaagga aagcaacgct cctctgaaat      497
gcttgtcttt tatgctggga ggtgaccata gggctctgct tttaaagata tggctgcttc      557
aaaggccaga gtcacaggaa ggacttcttc cagggagatt agtgggtgat gagaggagag      617
ttaaagtac ctcagtgcct tcttgtccac ggttttggtg agttttcact cttctaatagc      677
aagggtctca cactgtgaac cacttaggat gtgatcactt tcaggtggcc aggaatgttg      737
aatgtctttg gctcagttca tttaaaaaag atatctattt gaaagtcttc agagttgtac      797
tatatgtttc cagtacagga tctgtacata aaagtttctt tcctaaacca ttcaccaaga      857
gccaatatct aggcattttc ttggtagcac aaattttctt attgcttaga aaattgtcct      917
ccttgttatt tctgtttgta agacttaagt gagttaggct ttttaaggaaa gcaacgctcc      977
tctgaaatgc ttgtctttna tgctgggagg tgaccatagg gctctgcttt taaagatatg      1037
gctgcttcaa aggccagagt cacaggaagg acttcttcca gggagattag tgggtgatgga      1097
gaggagagtt aaaatgacct catgtccttc ttgtccacgg ttttggtgag ttttcaactc      1157
tctaatacaa gggcttcaca ctgtgaacca cttaggatgt gatcactttc aggtggccag      1217
gaatgttgaa tgtctttggc tcagttcatt taaaaaagat atctatttga aagttctcag      1277
agttgtacat atgtttcaca gtacaggatc tgtacataaaa agtttctttc ctaaaccatt      1337
caccaagagc caatatctag gcattttctt ggtagcacia attttcttat tgcttagaaa      1397
attgtcctcc ttgttatttc tgtttgtaag acttaagtga gttaggtctt taaggaaagc      1457
aacgctcctc tgaaatgctt gtcttttatg ctgggagggtg accatagggc tctgctttta      1517

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<210> 76
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 22..318

<221> sig_peptide

<222> 22..93

<223> Von Heijne matrix

score 4.6

seq FFIFCSLNTLLLG/GV

<221> polyA_signal

<222> 497..502

<221> polyA_site

<222> 516..526

<400> 76

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ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga ttt ctt cta      51
                               Met Lys Ser Ala Lys Leu Gly Phe Leu Leu
                               -20                               -15
aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg ggt ggt gtt      99
Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu Gly Gly Val
                               -10                               -5                               1
aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat ccc tgc aaa      147
Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys
                               5                               10                               15
ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga tat ttc      195
Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg Tyr Phe
                               20                               25                               30
ctac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc ggc tgt      243
Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser Gly Cys
                               35                               40                               45                               50
aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt gaa gta gcc      291
Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg Glu Val Ala
                               55                               60                               65
tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg tgaactcatg      338
Cys Val Ala Lys Tyr Lys Pro Pro Arg
                               70                               75
aagttgtctg ctgcaccatc cgaaataaag acacaagaaa attcagactg attttgaaat      398
ctttgtaata tttccataat gctttaagct tccatatgtt tgctattttc ctgaccctag      458
ttttgtcttt cctggaaatt aactgtatga tcattagaat gaaagagtct ttctgtcaaa      518
aaaaaaaaa                                                                526
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<210> 77

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..292

<221> sig_peptide

<222> 8..118

<223> Von Heijne matrix

score 5.6

seq WLLLDALLRLGDT/KK

<221> polyA_signal
<222> 317..322

<221> polyA_site
<222> 339..352

<400> 77

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ctgagat atg gca agt ccc gct gta aac agg tgg aaa agg cca agg ttg      49
      Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu
            -35                    -30                    -25

aag ccg gtg tgg cca cgg cgc ttg gaa tcc tgg ttg ttg ctg gat gct      97
Lys Pro Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala
            -20                    -15                    -10

ctt ttg cga tta gga gat acc aaa aaa aag cga cag cct gaa gca gcc     145
Leu Leu Arg Leu Gly Asp Thr Lys Lys Lys Arg Gln Pro Glu Ala Ala
            -5                    1                    5

aca aaa tcc tgt gtt aga agc agc tgt ggg ggt ccc agt gga gat ggg     193
Thr Lys Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly
10                    15                    20                    25

cct ccc cca tgc ctc cag cag cct gac cct cgt gcc ctg tct cag gcg     241
Pro Pro Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala
            30                    35                    40

ttc tct aga tcc ttt cct ctg ttt ccc tct ctc gct ggc aaa agt atg     289
Phe Ser Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met
            45                    50                    55

atc taattgaaac aagactgaag gatcaataaa cagccatctg ccccttcaaa     342
Ile

aaaaaaaaa                                                                352

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<210> 78

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 16..378

<221> sig_peptide

<222> 16..84

<223> Von Heijne matrix

score 9.8

seq FLLFFFLFLLTRG/SL

<221> polyA_signal

<222> 502..507

<221> polyA_site

<222> 522..542

<400> 78

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cacgacctgt gggcc atg atg cta ccc caa tgg ctg ctg ctg ctg ttc ctt      51
      Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu
            -20                    -15

```

```

ctc ttc ttc ttt ctc ttc ctc ctc acc agg ggc tca ctt tct cca aca      99
Leu Phe Phe Phe Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr
   -10                -5                1                5
aaa tat aac ctt ttg gag ctc aag gag tct tgc atc cgg aac cag gac      147
Lys Tyr Asn Leu Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp
                10                15                20
tgc gag act ggc tgc tgc caa cgt gct cca gac aat tgc gag tcg cac      195
Cys Glu Thr Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
                25                30                35
tgc gcg gag aag ggg tcc gag ggc agt ctg tgt caa acg cag gtg ttc      243
Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe
                40                45                50
ttt ggc caa tat aga gcg tgt ccc tgc ctg cgg aac ctg act tgt ata      291
Phe Gly Gln Tyr Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile
                55                60                65
tat tca aag aat gag aaa tgg ctt agc atc gcc tat ggc cgt tgt cag      339
Tyr Ser Lys Asn Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln
                70                75                80                85
aaa att gga agg cag aag ttg gct aag aaa atg ttc ttc tagtgctccc      388
Lys Ile Gly Arg Gln Lys Leu Ala Lys Lys Met Phe Phe
                90                95
tcctttcttgcc tgctctctcc tctctccacct gctctctctcc ctaccagag ctctgtgttc      448
accctgttcc ccagagcctc caccatgagt ggaggggaagt ggggagtgat tgaaataaag      508
agcttttttca atgaaaaaaaa aaaaaaaaaa aaaa      542

<210> 79
<211> 233
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..233

<400> 79
gcaaaaccaa aaccagcacc gatcccgaca tagatcagtg acgtcttttt cttcag atg      59
Met
1
atc cta tgt ttc ctt ctt cct cat cat cgt ctt cag gaa gcc aga cag      107
Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg Gln
                5                10                15
att caa gta ttg aag atg ctg cca agg gaa aaa tta aga aga aga gaa      155
Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg Glu
                20                25                30
gag aga aaa caa ata aat ggg aaa aaa gaa agg aca aaa tat gaa aca      203
Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu Thr
                35                40                45
cca aga aaa aga gaa gga aaa aaa aaa aaa      233
Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
50                55

<210> 80
<211> 660

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..340

<221> sig_peptide
<222> 83..124
<223> Von Heijne matrix
score 7.5
seq VALNLIILVPCCAA/WC

<221> polyA_signal
<222> 573..578

<221> polyA_site
<222> 607..660

<400> 80
gaatttgtaa aacttctgct cgtttacact gcacattgaa tacaggtaac taattggaag 60
gagaggggag atcactcttt tg atg gtg gcc ctg aac ctc att ctg gtt ccc 112
Met Val Ala Leu Asn Leu Ile Leu Val Pro
-10 -5
Tgc tgc gct gct tgg tgt gac cca cgg agg atc cac tcc cag gat gac 160
Cys Cys Ala Ala Trp Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp
1 5 10
Gtg ccc cgt agc tct gct gct gat act ggg tct gcg atg cag cgg cgt 208
Val Pro Arg Ser Ser Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg
15 20 25
gag gcc tgg gct ggt tgg aga agg tca caa ccc ttc tct gtt ggt ctg 256
Glu Ala Trp Ala Gly Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu
30 35 40
cct tct gct gaa aga ctc gag aac caa cca ggg aag ctg tcc tgg agg 304
Pro Ser Ala Glu Arg Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg
45 50 55 60
tcc ctg gtc gga gag gga tat aga atc tgt gac ctc tgacaactgt 350
Ser Leu Val Gly Glu Gly Tyr Arg Ile Cys Asp Leu
65 70
gaagccaccc tgggctacag aaaccacagt cttcccagca attattacaa ttcttgaatt 410
ccttggggat tttttactgc cttttcaaag cacttaagtg ttagatctaa cgtgttccag 470
tgtctgtctg aggtgactta aaaaatcaga acaaaacttc tattatccag agtcatggga 530
gagtacaccc tttccaggaa taatgttttg ggaaacactg aaatgaaatc ttcccagtat 590
tataaattgt gtatttaaaa aaagaaactt ttctgaatgc ctacctggcg gtgtatacca 650
ggcagtgtgc 660

<210> 81
<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..541

<221> sig_peptide
 <222> 47..220
 <223> Von Heijne matrix
 score 5.4
 seq QLLDSVLWLALG/LT

<221> polyA_site
 <222> 597..605

<400> 81

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aaagtgggag gagcactagg tcttcccgtc acctccacct ctctcc atg acc cgg      55
                               Met Thr Arg
ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg atc cca gtt cct      103
Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile Pro Val Pro
-55                               -50                               -45                               -40
cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt cca gtg cgt cca      151
Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro Val Arg Pro
                               -35                               -30                               -25
cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc ctg gac agt gtc      199
Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu Asp Ser Val
                               -20                               -15                               -10
cta tgg ctg ggg gca cta gga ctg aca atc cag gca gtc ttt tcc acc      247
Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val Phe Ser Thr
                               -5                               1                               5
act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc ctc acc ttt gac      295
Thr Gly Pro Ala Leu Leu Leu Leu Leu Val Ser Phe Leu Thr Phe Asp
10                               15                               20                               25
ctg ctc cat agg ccc gca ggt cac act ctg cca cag cgc aaa ctt ctc      343
Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg Lys Leu Leu
                               30                               35                               40
acc agg ggc cag agt cag ggg gcc ggt gaa ggt cct gga cag cag gag      391
Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly Gln Gln Glu
                               45                               50                               55
gct cta ctc ctg caa atg ggt aca gtc tca gga caa ctt agc ctc cag      439
Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu Ser Leu Gln
60                               65                               70
gac gca ctg ctg ctg ctg ctc atg ggg ctg ggc ccg ctc ctg aga gcc      487
Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu Leu Arg Ala
75                               80                               85
tgt ggc atg ccc ttg acc ctg ctt ggc ctg gct ttc tgc ctc cat cct      535
Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys Leu His Pro
90                               95                               100                               105
tgg gcc tgagagcccc tccccacaac tcagtgtcct tcaaataac aatgaccacc      591
Trp Ala
cttcttcaaa aaaa      605
  
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<210> 82
 <211> 396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..285

<221> sig_peptide
 <222> 46..150
 <223> Von Heijne matrix
 score 3.6
 seq LEPGLSSSAACNG/KE

<221> polyA_signal
 <222> 364..369

<221> polyA_site
 <222> 385..396

<400> 82
 cctctacagg aatcagactc agcctctttt ggttttcagt gaagt atg cct ttt caa 57
 Met Pro Phe Gln
 -35
 ttt gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca 105
 Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser
 -30 -25 -20
 att gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag 153
 Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys
 -15 -10 -5 1
 gag atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc 201
 Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys
 5 10 15
 ctg aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag 249
 Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys
 20 25 30
 cca cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt 295
 Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 35 40 45
 aagtccttttg tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct 355
 ggtaaacaaa taaaagtggg ggcaccttca aaaaaaaaaa a 396

<210> 83
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..240

<221> sig_peptide
 <222> 22..84
 <223> Von Heijne matrix
 score 12
 seq VLVLCVLLLQAQG/GY

<221> polyA_signal
 <222> 397..402

<221> polyA_site
 <222> 421..432

<400> 83

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gctcacgctc tggtcagagt t atg gca ccc cag act ctg ctg cct gtc ctg      51
                        Met Ala Pro Gln Thr Leu Leu Pro Val Leu
                        -20                                -15
gtt ctc tgt gtg ctg ctg ctg cag gcc cag gga gga tac cgt gac aag      99
Val Leu Cys Val Leu Leu Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys
-10                    -5                    1                    5
atg agg atg cag aga atc aag gtc tgt gag aag cga ccc agc ata gat      147
Met Arg Met Gln Arg Ile Lys Val Cys Glu Lys Arg Pro Ser Ile Asp
                        10                    15                    20
cta tgc atc cac cac tgt tca tgt ttc caa aag tgt gaa aca aat aag      195
Leu Cys Ile His His Cys Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys
                        25                    30                    35
ata tgc tgt tca gcc ttc tgt ggg aac att tgt atg agc atc cta      240
Ile Cys Cys Ser Ala Phe Cys Gly Asn Ile Cys Met Ser Ile Leu
                        40                    45                    50
tgagtgggag agtgggctgg gatgtgcatc ctgctccctg aacccttcca tccgagactg      300
tgccacatc cgaagcacia ggacatcaaa tcatcagcac aagaacatca acaggaatgc      360
caccctcccc agtgtctgaa ctccctgtcc ctgtcaaagt aaccagaaca aatgcccatg      420
aaaaaaaaaa aa                                                         432

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<210> 84

<211> 420

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 89..382

<221> polyA_site

<222> 408..420

<400> 84

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ggcttgctga ccccatgtc gcctctgtag gtagaagaag tatgtcttcc tggacccct      60
ggctgggtgct gtaacaaaga cccatgtg atg ctg ggg gca gag aca gag gag      112
                        Met Leu Gly Ala Glu Thr Glu Glu
                        1                    5
aag ctg ttt gat gcc ccc ttg tcc atc agc aag aga gag cag ctg gaa      160
Lys Leu Phe Asp Ala Pro Leu Ser Ile Ser Lys Arg Glu Gln Leu Glu
                        10                    15                    20
cag cag gtc cca gag aac tac ttc tat gtg cca gac ctg ggc cag gtg      208
Gln Gln Val Pro Glu Asn Tyr Phe Tyr Val Pro Asp Leu Gly Gln Val
                        25                    30                    35                    40
cct gag att gat gtt cca tcc tac ctg cct gac ctg ccc ggc att gcc      256
Pro Glu Ile Asp Val Pro Ser Tyr Leu Pro Asp Leu Pro Gly Ile Ala
                        45                    50                    55
aac gac ctc atg tac att gcc gac ctg ggc ccc ggc att gcc ccc tct      304
Asn Asp Leu Met Tyr Ile Ala Asp Leu Gly Pro Gly Ile Ala Pro Ser
                        60                    65                    70
gcc cct ggc acc att cca gaa ctg ccc acc ttc cac act gag gta gcc      352
Ala Pro Gly Thr Ile Pro Glu Leu Pro Thr Phe His Thr Glu Val Ala
                        75                    80                    85
gag cct ctc aag acc tac aag atg ggg tac taacagcacc accaccgccc      402
Glu Pro Leu Lys Thr Tyr Lys Met Gly Tyr

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90
ccaccaaaaa aaaaaaaaa

95

420

<210> 85
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..415

<221> sig_peptide
<222> 80..142
<223> Von Heijne matrix
score 5.4
seq TFCLIFGLGAVWG/LG

<221> polyA_signal
<222> 471..476

<221> polyA_site
<222> 488..501

<400> 85
cccgcttgat tccaagaacc tcttcgatat ttatttttat ttttaaagag ggagacgatg 60
gactgagctg atccgcacc atg gag tct cgg gtc tta ctg aga aca ttc tgt 112
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys
-20 -15
ttg atc ttc ggt ctc gga gca gtt tgg ggg ctt ggt gtg gac cct tcc 160
Leu Ile Phe Gly Leu Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser
-10 -5 1 5
cta cag att gac gtc tta aca gag tta gaa ctt ggg gag tcc acg acc 208
Leu Gln Ile Asp Val Leu Thr Glu Leu Gly Glu Ser Thr Thr
10 15 20
gga gtg cgt cag gtc ccg ggg ctg cat aat ggg acg aaa gcc ttt ctc 256
Gly Val Arg Gln Val Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu
25 30 35
ttt caa gat act ccc aga agc ata aaa gca tcc act gct aca gct gaa 304
Phe Gln Asp Thr Pro Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu
40 45 50
cag ttt ttt cag aag ctg aga aat aaa cat gaa ttt act att ttg gtg 352
Gln Phe Phe Gln Lys Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val
55 60 65 70
acc cta aaa cag acc cac tta aat tca gga gtt att ctc tca att cac 400
Thr Leu Lys Gln Thr His Leu Asn Ser Gly Val Ile Leu Ser Ile His
75 80 85
cac ttg gat cac agg taaatgtggt tgctggagtt tcctgtgttt tcattatatg 455
His Leu Asp His Arg
90
tggttaaattg aatatattaa agagaagtaa acaaaaaaaaa aaaaaa 501

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<211> 454
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<222> 152..361

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<222> 152..283
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score 4.7
seq FLLSLSLITYCFW/DP

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gtgttggttc cgcgtgcttc cgtcttgagt t atg tgc tgc tat tgt cgg ata 172
Met Cys Cys Tyr Cys Arg Ile
-40
ttt tgt ctt aga tgt acg tac ttt cct gtt cat tgt ggt atg tgt aat 220
Phe Cys Leu Arg Cys Thr Tyr Phe Pro Val His Cys Gly Met Cys Asn
-35 -30 -25
ttg cgt tac ttt gaa ttt tcc acg ttt tta ctt tct ttg tct ctc atc 268
Leu Arg Tyr Phe Glu Phe Ser Thr Phe Leu Leu Ser Leu Ser Leu Ile
-20 -15 -10
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Thr Tyr Cys Phe Trp Asp Pro Pro His Arg Gly Ser His Ser Leu Ser
-5 1 5 10
cta gag cac act ccc ttg gat ttc ctc gag tgg ggt ctg ctg cgg 361
Leu Glu His Thr Pro Leu Asp Phe Leu Glu Trp Gly Leu Leu Arg
15 20 25
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gtttcgttgt agcacattaa aaatattttc ccc 454

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<212> DNA
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<221> sig_peptide
<222> 32..70
<223> Von Heijne matrix
score 4.2
seq MLFSLSLLSNLNQ/IG

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<222> 1240..1245

<221> polyA_site
<222> 1261..1272

<400> 87

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Met Leu Phe Ser Leu Ser Leu

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ctc tcc aac ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac 100
Leu Ser Asn Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His

-5

1

5

10

att cct ggc caa tca gct cag ctg ttt att tac caa atg tct tca caa 148
Ile Pro Gly Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln

15

20

25

caa cta cag cag cag cct tcg gct aac aaa aaa gca gga aaa atc cac 196
Gln Leu Gln Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile His

30

35

40

aac acc ccc ttc gcc aac caa cta aat cca acg caa cat ctg gca aaa 244
Asn Thr Pro Phe Ala Asn Gln Leu Asn Pro Thr Gln His Leu Ala Lys

45

50

55

cct ttt cag caa att ctt cct ggc cgt cag tcc ggc agc ctc acc tca 292
Pro Phe Gln Gln Ile Leu Pro Gly Arg Gln Ser Gly Ser Leu Thr Ser

60

65

70

cca ttt cta gct tgc tgaaacccaa aactaatctc caagaaggag aagcttctct 347
Pro Phe Leu Ala Cys

75

cgcagccgga gcaggtccct ttctagagat aggagaagag agagatcgct gtctcgggag 407
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<222> 114..239

<223> Von Heijne matrix

score 5.2

seq LLFDLVCHEFCQS/DD

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<221> polyA_site
<222> 793..804

<400> 88

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                                     Met
cac att tta caa ctg ctt act aca gtg gat gat gga att caa gca att      164
His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile
-40 -35 -30
gta cat tgt cct gac act gga aaa gac att tgg aat tta ctt ttt gac      212
Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp
-25 -20 -15 -10
ctg gtc tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt      260
Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu
-5 1 5
caa gaa cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc      308
Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala
10 15 20
atc tat gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta      356
Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val
25 30 35
gat ctt cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa      404
Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu
40 45 50 55
cag tgt cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa      452
Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu
60 65 70
act aaa agg act gat tta acc caa gat gat ctc cac ttg aaa atc tta      500
Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile Leu
75 80 85
aag gat att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca      548
Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr
90 95 100
aag gag acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag      596
Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln
105 110 115
aag tgt tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg      644
Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val
120 125 130 135
gtg gaa gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct      692
Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala
140 145 150
gat gac ttg gaa aaa aac ttc cca agt ttg aag gtt cag act      734
Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
155 160 165
taaaacctga attggaatta cttctgtaca agaaataaac tttatttttc tcactgacaa      794
aaaaaaaaa      804

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<222> 780..785

<221> polyA_site

<222> 791..802

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tgctgcaaga tctgttatcc gctctgtggt tttgtcatcc ttgctgcctg tgttgtggcc      180
tgtgttggtc tggtgtgg atg cag gtt gct ctc aag gag gat ctg gat gcc      231
                Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala
                1          5          10
ctc aag gaa aaa ttt cga aca atg gaa tct aat cag aaa agc tca ttc      279
Leu Lys Glu Lys Phe Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe
                15          20          25
Caa gaa atc ccc aaa ctt aat gaa gaa cta ctc agc aag caa aaa caa      327
Gln Glu Ile Pro Lys Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln
                30          35          40
ctt gag aag att gaa tct gga gag atg ggt ttg aac aaa gtc tgg ata      375
Leu Glu Lys Ile Glu Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile
                45          50          55
aac atc aca gaa atg aat aag cag att tct ctg ttg act tct gca gtg      423
Asn Ile Thr Glu Met Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val
                60          65          70          75
aac cac ctc aaa gcc aat gtt aag tca gct gca gac ttg att agc ctg      471
Asn His Leu Lys Ala Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu
                80          85          90
ccct acc act gta gag gga ctt cag aag agt gta gct tcc att ggc aat      519
Pro Thr Thr Val Glu Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn
                95          100          105
act tta aac agc gtc cat ctt gct gtg gaa gca cta cag aaa act gtg      567
Thr Leu Asn Ser Val His Leu Ala Val Glu Ala Leu Gln Lys Thr Val
                110          115          120
gat gaa cac aag aaa acg atg gaa tta ctg cag agt gat atg aat cag      615
Asp Glu His Lys Lys Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln
                125          130          135
cac ttc ttg aag gag act cct gga agc aac cag atc att ccg tca cct      663
His Phe Leu Lys Glu Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro
                140          145          150          155
tca gcc aca tca gaa ctt gac aat aaa acc cac agt gag aat ttg aaa      711
Ser Ala Thr Ser Glu Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys
                160          165          170
cag atg ggt gat aga tct gcc act ctg aaa aga cag tct ttg gac caa      759
Gln Met Gly Asp Arg Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln
                175          180          185
gtc acc aac aga aca gat aca gta aaa atc caa aaa aaa a      802
Val Thr Asn Arg Thr Asp Thr Val Lys Ile Gln Lys Lys Lys
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 <211> 1490
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 <213> Homo sapiens

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<221> sig_peptide
 <222> 38..148
 <223> Von Heijne matrix
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 seq LLSACLVTWGLG/EP

<221> polyA_signal
 <222> 1452..1457

<221> polyA_site
 <222> 1478..1490

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                                     Met Pro His Ser Ser Leu
                                     -35
cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc cag aag gca gcc      103
His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala Gln Lys Ala Ala
-30 -25 -20
ctg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg ggg cta gga gag      151
Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp Gly Leu Gly Glu
-15 -10 -5 1
cca cca gag cac act ctc cgg tac ctg gtc ctc cac cta gcc tcc ctg      199
Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His Leu Ala Ser Leu
5 10 15
cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg gct gag gag ctg      247
Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu Ala Glu Glu Leu
20 25 30
cgc cac atc cac tcc agg tac cgg ggc agc tac tgg agg act gtg cgg      295
Arg His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp Arg Thr Val Arg
35 40 45
gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg ttg ctg ctg tcc      343
Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu Leu Leu Leu Ser
50 55 60 65
atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc ccg ccc ttc act      391
Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly Pro Pro Phe Thr
70 75 80
tgg atg ctt gcc ctc ctg ggc ctc tcg cag gca ctg aac atc ctc ctg      439
Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile Leu Leu
85 90 95
ggc ctc aag ggc ctg gcc cca gct gag atc tct gca gtg tgt gaa aaa      487
Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys Glu Lys
100 105 110
ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca tat tac atc gga      535
Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly
115 120 125
tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg att cga act tac      583
    
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Tyr	Leu	Arg	Leu	Ile	Leu	Pro	Glu	Leu	Gln	Ala	Arg	Ile	Arg	Thr	Tyr	
130					135					140					145	
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Asn	Gln	His	Tyr	Asn	Asn	Leu	Leu	Arg	Gly	Ala	Val	Ser	Gln	Arg	Leu	
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tat	att	ctc	ctc	cca	ttg	gac	tgt	ggg	gtg	cct	gat	aac	ctg	agt	atg	679
Tyr	Ile	Leu	Leu	Pro	Leu	Asp	Cys	Gly	Val	Pro	Asp	Asn	Leu	Ser	Met	
				165				170					175			
gct	gac	ccc	aac	att	cgc	ttc	ctg	gat	aaa	ctg	ccc	cag	cag	acc	ggg	727
Ala	Asp	Pro	Asn	Ile	Arg	Phe	Leu	Asp	Lys	Leu	Pro	Gln	Gln	Thr	Gly	
				180			185					190				
gac	cgt	gct	ggc	atc	aag	gat	cgg	gtt	tac	agc	aac	agc	atc	tat	gag	775
Asp	Arg	Ala	Gly	Ile	Lys	Asp	Arg	Val	Tyr	Ser	Asn	Ser	Ile	Tyr	Glu	
				195		200					205					
ctt	ctg	gag	aac	ggg	cag	cgg	gcg	ggc	acc	tgt	gtc	ctg	gag	tac	gcc	823
Leu	Leu	Glu	Asn	Gly	Gln	Arg	Ala	Gly	Thr	Cys	Val	Leu	Glu	Tyr	Ala	
210				215						220					225	
acc	ccc	ttg	cag	act	ttg	ttt	gcc	atg	tca	caa	tac	agt	caa	gct	ggc	871
Thr	Pro	Leu	Gln	Thr	Leu	Phe	Ala	Met	Ser	Gln	Tyr	Ser	Gln	Ala	Gly	
				230					235					240		
ttt	agc	cgg	gag	gat	agg	ctt	gag	cag	gcc	aaa	ctc	ttc	tgc	cgg	aca	919
Phe	Ser	Arg	Glu	Asp	Arg	Leu	Glu	Gln	Ala	Lys	Leu	Phe	Cys	Arg	Thr	
				245				250					255			
ctt	gag	gac	atc	ctg	gca	gat	gcc	cct	gag	tct	cag	aac	aac	tgc	cgc	967
Leu	Glu	Asp	Ile	Leu	Ala	Asp	Ala	Pro	Glu	Ser	Gln	Asn	Asn	Cys	Arg	
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ctc	att	gcc	tac	cag	gaa	cct	gca	gat	gac	agc	agc	ttc	tcg	ctg	tcc	1015
Leu	Ile	Ala	Tyr	Gln	Glu	Pro	Ala	Asp	Asp	Ser	Ser	Phe	Ser	Leu	Ser	
				275			280						285			
cag	gag	gtt	ctc	cgg	cac	ctg	cgg	cag	gag	gaa	aag	gaa	gag	gtt	acc	1063
Gln	Glu	Val	Leu	Arg	His	Leu	Arg	Gln	Glu	Glu	Lys	Glu	Glu	Val	Thr	
				290		295				300					305	
gtg	ggc	agc	ttg	aag	acc	tca	gcg	gtg	ccc	agt	acc	tcc	acg	atg	tcc	1111
Val	Gly	Ser	Leu	Lys	Thr	Ser	Ala	Val	Pro	Ser	Thr	Ser	Thr	Met	Ser	
				310				315						320		
caa	gag	cct	gag	ctc	ctc	ctc	agt	gga	atg	gga	aag	ccc	ctc	cct	ctc	1159
Gln	Glu	Pro	Glu	Leu	Leu	Leu	Ser	Gly	Met	Gly	Lys	Pro	Leu	Pro	Leu	
				325				330					335			
cgc	acg	gat	ttc	tct	tgagacccag	gggcaccagg	ccagagcctc	cagtgggtctc								1214
Arg	Thr	Asp	Phe	Ser												
				340												
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<211> 361

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<213> Homo sapiens

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<400> 91

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Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr Tyr	
10 15 20 25	
cgc gac tgg ctg ctg cgg cgc gag gat gtt tta gaa gaa tgt atg tct	148
Arg Asp Trp Leu Leu Arg Arg Glu Asp Val Leu Glu Glu Cys Met Ser	
30 35 40	
ctt ccc aag cta tct tct tat tct gga tgg gtg gta gag cac gtc cta	196
Leu Pro Lys Leu Ser Ser Tyr Ser Gly Trp Val Val Glu His Val Leu	
45 50 55	
ccc cat atg cag gag aac caa cct ctg tct gag act tcg cca tcc tct	244
Pro His Met Gln Glu Asn Gln Pro Leu Ser Glu Thr Ser Pro Ser Ser	
60 65 70	
acg tca gct tca gcc cta gat caa ccc tca ttt gtt ccc aaa tct cct	292
Thr Ser Ala Ser Ala Leu Asp Gln Pro Ser Phe Val Pro Lys Ser Pro	
75 80 85	
gac gca agc tct gcc ttt tcc cca gcc tcc cct gca aca cca aat gga	340
Asp Ala Ser Ser Ala Phe Ser Pro Ala Ser Pro Ala Thr Pro Asn Gly	
90 95 100 105	
acc aag ggc aaa aaa aaa aaa	361
Thr Lys Gly Lys Lys Lys Lys	
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<213> Homo sapiens

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<222> 591..605

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1 5 10 15	
agc tcc cta gaa tct cct gga atg ctt aat gga cct ttc cag cac cga	95
Ser Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg	
20 25 30	
aat tca aga att atg act cat cgg tca gca gaa aag tgaggatacc	141
Asn Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys	
35 40	
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catatgtagc ttctcaggat gttaattctg ttctctctgt gttggtgtct gagcaccag	261
aaggtagagc caggggcact tataaaccag gagcattatt tgacaggcac ttaagaaaga	321

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Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys		
	-5	1
gag ccc act cag cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg		149
Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp		
	10	15
aat aag aaa ggc aac gtt ttg cag ctt cca aat ttc tgaagaaact		195
Asn Lys Lys Gly Asn Val Leu Gln Leu Pro Asn Phe		
	25	30
aatctcagat tggcagttaa agtcaaaaatg ttgccaaata tttatttcctt ttgcctaagt		255
ttggctaccc ggttcaattg ctttttattt ttaatgtctt gactcttcag agttcgtacc		315
tcaaaagaac aatgagaaca tttgctttgc tttctgctga atccctaatac tcaacaatct		375
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tgccaggagc tccttccttc tagcaatttc tactaaaatg tccaagtaga atgtttcctt		495
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<210> 94
 <211> 1150
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> 184..915

<221> sig_peptide
<222> 184..237
<223> Von Heijne matrix
score 3.5
seq LLGLELSEAEAG/AD

<221> polyA_signal
<222> 1119..1124

<221> polyA_site
<222> 1139..1150

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<400> 94
cggatttgac gatggtgttc ggtcttgaat ggaaatgtag tcttaggcc gtcttaggtt      60
tttgaacagg atagtaggta tccgagtcg attgagggcc agagcaggca ctggggttcg      120
gatcctgggc aaagtgtccc acgttgaggg tctcgaggac gcctagatct ctttcccagg      180
gcc atg gcg aac ccg aag ctg ctg gga ctg gag cta agc gag gcg gag      228
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
      -15      -10      -5
gcg atc ggt gct gat tcg gcg cga ttt gag gag ctg ctg ctg cag gcc      276
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
      1      5      10
tcg aag gag ctc cag caa gcc cag aca acc aga cca gaa tcg aca caa      324
Ser Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln
      15      20      25
atc cag cct cag cct ggt ttc tgc ata aag acc aac tcc tcg gaa ggg      372
Ile Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly
      30      35      40      45
aag gtt ttc atc aac atc tgc cac tcc ccc tct atc cct cct ccc gcc      420
Lys Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala
      50      55      60
gac gtg acc gag gag gag ctg ctt cag atg cta gag gag gac caa gct      468
Asp Val Thr Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala
      65      70      75
ggg ttt cgc atc ccc atg agt ctg gga gag cct cat gca gaa ctg gat      516
Gly Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp
      80      85      90
gca aaa ggc cag gga tgt acc gcc tac gac gta gct gtc aac agc gac      564
Ala Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp
      95      100      105
ttc tac cgg agg atg cag aac agc gat ttc ttg cgg gag ctc gtg atc      612
Phe Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile
      110      115      120      125
acc atc gcc agg gag ggc ctt gag gac ata tac aac ttg cag ctg aat      660
Thr Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn
      130      135      140
ccg gaa tgg cgc atg atg aag aac cgg cca ttc atg ggc tcc atc tcg      708
Pro Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser
      145      150      155
cag cag aac atc cgc tcg gag cag cgt cct cgg atc cag gag ctg ggg      756
Gln Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly
      160      165      170
gac ctg tac acg ccc gcc ccc ggg aga gct gag tca ggg cct gaa aag      804

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Asp	Leu	Tyr	Thr	Pro	Ala	Pro	Gly	Arg	Ala	Glu	Ser	Gly	Pro	Glu	Lys	
175						180					185					
cct	cac	ctg	aac	ctg	tgg	ctg	gaa	gcc	ccc	gac	ctc	ctc	ttg	gcc	gaa	852
Pro	His	Leu	Asn	Leu	Trp	Leu	Glu	Ala	Pro	Asp	Leu	Leu	Leu	Ala	Glu	
190					195				200					205		
ggt	gac	ctc	ccc	aaa	ctg	gat	gga	gcc	ctg	ggg	ctg	tcg	ctg	gag	atc	900
Val	Asp	Leu	Pro	Lys	Leu	Asp	Gly	Ala	Leu	Gly	Leu	Ser	Leu	Glu	Ile	
			210				215				220					
ggg	aga	acc	gcc	tgg	tgatgggggg	ccccagcag	ctgtatcatc	tagacgctta								955
Gly	Arg	Thr	Ala	Trp												
			225													
tatccccgccg	cagatcaact	ctcatgagag	caaggcagcc	ttccaccgga	agagaaagca											1015
attaatggtg	gccatgccgc	ttctgccggt	gccttcttga	tcagggtgtc	tccttgtgct											1075
tctgagatgt	ggagaagagg	ctgctggcct	ccctaaaagt	tgaaataaaa	gatttttggc											1135
tttaaaaaaaa	aaaaa															1150

<210> 95

<211> 1513

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..1116

<221> sig_peptide

<222> 58..159

<223> Von Heijne matrix

score 4

seq IAVLYLHLYDVFG/DP

<221> polyA_signal

<222> 1486..1491

<221> polyA_site

<222> 1504..1513

<400> 95

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atg	gag	aga	ggc	ctg	aaa	tca	gca	gac	cct	cgg	gat	ggc	acc	ggt	tac	105
Met	Glu	Arg	Gly	Leu	Lys	Ser	Ala	Asp	Pro	Arg	Asp	Gly	Thr	Gly	Tyr	
			-30						-25					-20		
act	ggc	tgg	gca	ggt	att	gct	gtg	ctt	tac	tta	cat	ctt	tat	gat	gta	153
Thr	Gly	Trp	Ala	Gly	Ile	Ala	Val	Leu	Tyr	Leu	His	Leu	Tyr	Asp	Val	
			-15						-10					-5		
ttt	ggg	gac	cct	gcc	tac	cta	cag	tta	gca	cat	ggc	tat	gta	aag	caa	201
Phe	Gly	Asp	Pro	Ala	Tyr	Leu	Gln	Leu	Ala	His	Gly	Tyr	Val	Lys	Gln	
	1			5					10							
agt	ctg	aac	tgc	tta	acc	aag	cgc	tcc	atc	acc	ttc	ctt	tgt	ggg	gat	249
Ser	Leu	Asn	Cys	Leu	Thr	Lys	Arg	Ser	Ile	Thr	Phe	Leu	Cys	Gly	Asp	
15			20						25				30			
gca	ggc	ccc	ctg	gca	gtg	gcc	gct	gtg	cta	tat	cat	aag	atg	aac	aat	297
Ala	Gly	Pro	Leu	Ala	Val	Ala	Ala	Val	Leu	Tyr	His	Lys	Met	Asn	Asn	
			35					40					45			
gag	aag	cag	gca	gaa	gat	tgc	atc	aca	cgg	cta	att	cac	cta	aat	aag	345

[illegible]

gaaactcaat acagataaag ataaatatgt gactattaaa aaaaaaa

1513

<210> 96
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 327..416

<221> polyA_site
<222> 404..417

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tcttgcaaaa atggttctgt gcacttggat gtgaaatgct gtccagtttt atttttttta 120
tggtgttatc ctctgatgta caaaaaattc agaaaatgat ctctgtagat attctgtttt 180
attttgggtca tctttagaag ttatcaggaa tgtgttttaa acaagaagag aacttttcta 240
aggaatgata catagaaaag atttttatattt aaaatgagtt gtaaagcttg tgtttctttg 300
tttgctgcaag ctatctgccc aagtta atg caa atg gac aca ttt ttt atg tca 353
Met Gln Met Asp Thr Phe Phe Met Ser
1 5
gaa aaa cac aca cac aca cac aca cat ata cac aca cac aca cga aaa 401
Glu Lys His Thr His Thr His Thr His Ile His Thr His Thr Arg Lys
10 15 20 25
aca aaa aaa aaa aaa a 417
Thr Lys Lys Lys Lys
30

<210> 97
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..398

<221> sig_peptide
<222> 63..206
<223> Von Heijne matrix
score 4.9
seq PSLAAGLLFGSLA/GL

<400> 97
ggggccttcg tgagaccggt gcaggccttg ggtagtctcc tgtctggaca gagaagagaa 60
aa atg cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt 107
Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe
-45 -40 -35
ggc tac gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa 155
Gly Tyr Ala Ala Leu Val Ala Ser Gly Ile Ile Gly Tyr Val Lys
-30 -25 -20

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gca ggc agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta      203
Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
      -15                      -10                      -5
gcc ggc ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg      251
Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp
      1                      5                      10                      15
gtt ttc cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg      299
Val Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg
                        20                      25                      30
ttc tac cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc      347
Phe Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala
                        35                      40                      45
agt ttg ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc      395
Ser Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro
                        50                      55                      60
cat tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca      448
His
tcttccacta ttttcaatat attaagagaa ataagtgcag cattttttgca tctgacattt      508
tacctaaaaa aaaagacacc aaacttggca gagaggtgga aaatcagtca tgattacaaa      568
cctacagagg tggcgagtat gtaacacaag agctt      603

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<210> 98
<211> 522
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 2..163
<221> polyA_signal
<222> 488..493
<221> polyA_site
<222> 511..522

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<400> 98
c gag att gcg ggc tat ggc gcc gaa ggt ttt tcg tca gta ctg gga tat      49
Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
      1                      5                      10                      15
ccc cga tgg cac cga ttg cca ccg caa agc cta cag cac cac cag tat      97
Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
                        20                      25                      30
tgc cag cgt cgc tgg cct gac cgc cgc tgc cta cag agt cac act caa      145
Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
                        35                      40                      45
tcc tcc ggg cac ctt cct nntgaaggag tggctaagggt tggacaatac      193
Ser Ser Gly His Leu Pro
      50
acgttactg cagctgctgt cggggccgtg tttggcctca ccacctgcat cagcgcccat      253
gtccgcgaga agcccagcga cccctgaac tacttccccg gtggctgcgc cnggaggcct      313
gactctggga gcacgcacgc acaactacgg gattggcgcc gccgcctgcg tgtactttgg      373
catagcggcc tccctggtca agatggggcc gctggagggg tgggaggtgt ttgcaaaacc      433
caaggtgtga gccctgtgcc tgccggggacc tccagcctgc agaatgcgtc cagaaataaa      493
ttctgtgtct gtgtgtgaaa aaaaaaaaaa      522

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<210> 99
 <211> 956
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..465

<221> sig_peptide
 <222> 13..75
 <223> Von Heijne matrix
 score 3.9
 seq PVAVTAAVAPVLS/IN

<400> 99

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ngagtcggga aa atg gct gcg agt acn tcn atg gnc ccg gtg gct gtg acg      51
      Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr
              -20              -15              -10
gcg gca gtg gcg cct gtc ctg tcc ata aac agc gat ttc tca gat ttg      99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
              -5              1              5
cgg gaa att aaa aag caa ctg ctg ctt att gcg ggc ctt acc cgg gag      147
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
      10              15              20
cgg ggc cta cta cac agt agc aaa tgg tgc gcg gag ttg gct ttc tct      195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
      25              30              35              40
ctc cct gca ttg cct cnt ggc cag ctg caa ccg cct ccg cct att aca      243
Leu Pro Ala Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr
              45              50              55
gag gaa gat gcc cag gat atg gat gcc tat acc ctg gcc aag gcc tac      291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
              60              65              70
ttt gac gtt aaa gag tat gat cgg gca gca cat ttc ctg cat ggc tgc      339
Phe Asp Val Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys
              75              80              85
aat agc aag aaa gcc tat ttt ctg tat atg tat tcc aga tat ctg gtg      387
Asn Ser Lys Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val
              90              95              100
agg gcc att tta aaa tgt cat tct gcc ttt agt gaa aca tcc ata ttt      435
Arg Ala Ile Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe
      105              110              115              120
aga acc aat gga aaa gtt aaa tct ttt aaa tagcttagca gtgggccact      485
Arg Thr Asn Gly Lys Val Lys Ser Phe Lys
              125              130
gaatgaatgt actttataca tagcaataat aaaaaaaga tatcataaat aaagttaaaa      545
aggatggtag agaagaaaat attcttagga atgactaaca ggataagtaa caacctgatt      605
atttatattac tttaggttat ataaggttct tcatgcctgt gaattaatat tattgtgtaa      665
gaattaagtt aaaaagcctg ggctgacttt taaatttata aattcattta tcatgtttat      725
agtatatatta ttgtttttct ttcattggcta ttaaaaagta tgactgtaaa ggacaatgca      785
agnaaaccaa cttataactg tattgaataa taagtacaat ttattatttt actttgaaac      845
attatgaatt tactttccta ctttttctta gttgttatct atataaattg attaaaaaaa      905
cattttatgt acntnncatt tcctagtaca ggttgagtat cccttatttg a      956
  
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<210> 100
 <211> 1041
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..703

<221> sig_peptide
 <222> 20..94
 <223> Von Heijne matrix
 score 3.9
 seq ATVGLLMLGVTLN/NS

<221> polyA_signal
 <222> 1000..1005

<221> polyA_site
 <222> 1023..1041

<400> 100

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cagggtcctg catcctacc atg tcg atg gct gtg gaa acc ttt ggc ttc ttc      52
      Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe
      -25                -20                -15

atg gca act gtg ggg ctg ctg atg ctg ggg gtg act ctg cca aac agc      100
Met Ala Thr Val Gly Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser
      -10                -5                1

tac tgg cga gtg tcc act gtg cac ggg aac gtc atc acc acc aac acc      148
Tyr Trp Arg Val Ser Thr Val His Gly Asn Val Ile Thr Thr Asn Thr
      5                10                15

atc ttc gag aac ctc tgg ttt agc tgt gcc acc gac tcc ctg ggc gtc      196
Ile Phe Glu Asn Leu Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val
      20                25                30

tac aac tgc tgg gag ttc ccg tcc atg ctg gcc ctc tct ggg tat att      244
Tyr Asn Cys Trp Glu Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile
      35                40                45                50

cag gcc tgc cgg gca ctc atg atc acc gcc atc ctc ctg ggc ttc ctc      292
Gln Ala Cys Arg Ala Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu
      55                60                65

ggc ctc ttg cta ggc ata gcg ggc ctg cgc tgc acc aac att ggg ggc      340
Gly Leu Leu Leu Gly Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly
      70                75                80

ctg gag ctc tcc agg aaa gcc aag ctg gcg gcc acc gca ggg gcc ccc      388
Leu Glu Leu Ser Arg Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro
      85                90                95

cac att ctg gcc ggt atc tgc ggg atg gtg gcc atc tcc tgg tac gcc      436
His Ile Leu Ala Gly Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala
      100                105                110

ttc aac atc acc cgg gac ttc ttc gac ccc ttg tac ccc gga acc aag      484
Phe Asn Ile Thr Arg Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys
      115                120                125                130

tac gag ctg ggc ccc gcc ctc tac ctg ggg tgg agc gcc tca ctg atc      532
Tyr Glu Leu Gly Pro Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile
    
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	135	140	145	
tcc atc ctg ggt ggc ctc tgc ctc tgc tcc gcc tgc tgc tgc ggc tct				580
Ser Ile Leu Gly Gly Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser				
	150	155	160	
gac gag gac cca gcc gcc agc gcc cgg cgg ccc tac cag gct cca gtg				628
Asp Glu Asp Pro Ala Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val				
	165	170	175	
tcc gtg atg ccc gtc gcc acc tcg gac caa gaa ggc gac agc agc ttt				676
Ser Val Met Pro Val Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe				
	180	185	190	
ggc aaa tac ggc aga aac gcc tac gtg tagcagctct ggcccgtggg				723
Gly Lys Tyr Gly Arg Asn Ala Tyr Val				
195	200			
ccccgctgtc ttcccaactgc cccaaggaga ggggacctgg ccggggccca ttcccctata				783
gtaacctcag gggccggcca cgccccgctc ccgtagcccc gccccggcca cggccccgtg				843
tcttgcactc tcatggcccc tccaggccaa gaactgctct tgggaagtcg catatctccc				903
ctctgaggct ggatccctca tcttctgacc ctgggttctg ggctgtgaag gggacggtgt				963
ccccgcacgt ttgtattgtg tataaataca ttcattaata aatgcatatt gtgaccgtta				1023
aaaaaaaaa aaaaaaaaa				1041

<210> 101
 <211> 558
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 103..294
 <221> sig_peptide
 <222> 103..243
 <223> Von Heijne matrix
 score 5.9
 seq TWLGLLSFQNLHC/FP

<400> 101	
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taacattaac ttccttaagt aataatcaat gaaagaaatt ct atg cat ggt ttt	114
	Met His Gly Phe
	-45
gaa ata ata tcc ttg aaa gag gaa tca cca tta gga aag gtg agt cag	162
Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly Lys Val Ser Gln	
	-40 -35 -30
ggt cct ttg ttt aat gtg act agt ggc tca tca tca cca gtg acc tgg	210
Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser Pro Val Thr Trp	
	-25 -20 -15
ttg ggc cta ctc tcc ttc cag aac ctg cat tgc ttc cca gac ctc ccc	258
Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe Pro Asp Leu Pro	
	-10 -5 1 5
act gag atg cct cta aga gcc aaa gga gtc aac act tgagcctagg	304
Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr	
	10 15
gtgggctaca acaaaagatt ctaatttacc ttgcttcac taggtccagg ccccaagtag	364
cttgctgaag gaacttaaaa agtagctgtt atttattgta ttgtataagc taaaaacatt	424
tatttttgtt gaatcgaaac aattccatgt agcaatcttt tttctgttca cgggtgtttgt	484

gatagaacct taaattccgc aagcatcagt tttttgaaaa aatgggaatt gaccggatag 544
taacaggcaa agtt 558

<210> 102
<211> 730
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..518

<221> sig_peptide
<222> 81..173
<223> Von Heijne matrix
score 3.9
seq ILFHGVFYAGGFA/IV

<400> 102
ctcgtcatgc tctttgtagc gtggtgcttc tgttgctcac aggacaactt gcctttgatg 60
atttttcaaga gagttgtgct atg atg tgg caa aag tat gca gga agc agg cgg 113
Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg
-30 -25
tca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc 161
Ser Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
-20 -15 -10 -5
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg 209
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
1 5 10
gct tta tat tac aag ttg gca gtg gag cag ctg cag agc cat ccc gag 257
Ala Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu
15 20 25
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc 305
Ala Gln Glu Ala Leu Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu
30 35 40
atc gac agg gaa aac ttc gtg gac att gtt gat gcc aag ttg aag att 353
Ile Asp Arg Glu Asn Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile
45 50 55 60
cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac gtc cac tca tcc 401
Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser
65 70 75
aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag gtc ttt tta gag 449
Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu
80 85 90
ctc aag gat ggt cag cag att cct gtg ttc aag ctc agt ggg gaa aac 497
Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn
95 100 105
ggt gat gaa gtg aaa aag gag tagagacgac ccagaagacc cagcttgctt 548
Gly Asp Glu Val Lys Lys Glu
110 115
ctagtcctac cttccctcat ctctaccata tggccactgg ggtggtggcc catctcagtg 608
acagacactc ctgcaacca gttttccagc caccagtggg atgatggtat gtgccagcac 668
atggttaattt tgggtgtaatt ctaacttggg cacaacgaat gctattttgtc atttttaaac 728
tg 730

<210> 103
<211> 1098
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..326

<221> polyA_signal
<222> 1066..1071

<221> polyA_site
<222> 1087..1098

<400> 103
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ctctc atg gag ttg gct ccg aca gcc cgt ctg cca cca ggc cat ggt tcc 110
Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser
1 5 10 15
ttg ccc cat ggt gtc ctg gga ccc aga gca aca gga tct gtc acc cac 158
Leu Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His
20 25 30
ctc tct ctt ctc ccc cag atc aag caa cgt gcc tca gag gct ttg ccc 206
Leu Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro
35 40 45
gaa ttg ctt cgt cct gtc acc ccc atc acc aat ttt gag ggc agc cag 254
Glu Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln
50 55 60
tct cag gac cac agt gga atc ttt ggc ctg gta aca aac ctg gaa gag 302
Ser Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu
65 70 75
ctg gag gtg gac gat tgg gag ttc tgagcctctg caaactgtgc gcattctcca 356
Leu Glu Val Asp Asp Trp Glu Phe
80 85
gccagggatg cagaggccac ccagaggccc ttcttgaggg ccggccacat tcccgccttc 416
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aagaaaatcc tggagagata cttcactgct ccaaggcttt tgagacacaa gggaatctca 536
acaaccaggg atcaggaggg tccaaagccg acattcccag tctgtgagc tcaggtgacc 596
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tcttagcgcc tctgccagc tgccctggtg ctttctccaa gggccatcag tgtcttgcc 1016
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tcagagacgc aaaaaaaaaa aa 1098

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seq LLLLLITPSPSPL/LF

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atttttcctc ctagttctta gcttgcttct gcattgattg gctttacaca actggcattt 120
agtctgcatt acacaaaatag acactaattt atttgaaca agcagcaaa atg aga act 178
Met Arg Thr
-25
tta ttt ggt gca gtc agg gct cca ttt agt tcc ctc act ctg ctt cta 226
Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr Leu Leu Leu
-20 -15 -10
atc acc cct tct ccc agc cct ctt cta ttt gat aga ggt ctg tcc ctc 274
Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly Leu Ser Leu
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aga tca gca atg tct tagccctct cctctcttcc attccttcc gttggtactc 329
Arg Ser Ala Met Ser
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Met Gly Ser Leu Ser Gly
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ctg cgc ctg gca gca gga agc tgt ttt agg tta tgt gaa aga gat gtt 101
Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val
10 15 20
tcc tca tct cta agg ctt acc aga agc tct gat ttg aag aga ata aat 149
Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn
25 30 35
gga ttt tgc aca aaa cca cag gaa agt ccc gga gct cca tcc cgc act 197
Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr

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      40              45              50
tac aac aga gtg cct tta cac aaa cct acg gat tgg cag aaa aag atc      245
Tyr Asn Arg Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile
55              60              65              70
ctc ata tgg tca ggt cgc ttc aaa aag gaa gat gaa atc cca gag act      293
Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu Asp Glu Ile Pro Glu Thr
      75              80              85
gtc tcg ttg gag atg ctt gat gct gca aag aac aag atg cga gtg aag      341
Val Ser Leu Glu Met Leu Asp Ala Ala Lys Asn Lys Met Arg Val Lys
      90              95              100
agc agc tat cta atg att gcc ctg acg gtg gta gga tgc atc ttc atg      389
Ser Ser Tyr Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met
      105              110              115
gtt att gag ggc aag aag gct gcc caa aga cac gag act tta aca agc      437
Val Ile Glu Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser
      120              125              130
ttg aac tta gaa aag aaa gct cgt ctg aaa gag gaa gca gct atg aag      485
Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys Glu Glu Ala Ala Met Lys
      135              140              145              150
gcc aaa aca gag tagcagaggt atccgtgttg gctggatttt gaaaatccag      537
Ala Lys Thr Glu
gaattatgtt ataacgtgcc tgtattaaaa aggatgtggt atgaggatcc atttcataaa      597
gtatgatttg cccaaacctg taccatttcc gtatttctgc cgtagaagta gaaataaatt      657
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<221> polyA_site
<222> 542..554

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Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly
      1              5              10
act gtt atc act cca gat aca tgg aaa gat ggt gct agg aat acc aca      98
Thr Val Ile Thr Pro Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr
      15              20              25
gaa agt ggt gga aga aag ctg aat aaa aat aaa gct ttg act tca aaa      146
Glu Ser Gly Gly Arg Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys
      30              35              40
aaa gca aga ttt gat cca tat gga aag aat aag ttc tcc act tgt aga      194
Lys Ala Arg Phe Asp Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg
      45              50              55
att tgt aaa agt tct gtg cac caa cca ggt tct cat tac tgc cag ggc      242
Ile Cys Lys Ser Ser Val His Gln Pro Gly Ser His Tyr Cys Gln Gly

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Cys Ala Tyr Lys Lys Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu				
	80	85	90	
gat acc aaa aac tac aag caa aca tct gtc tagatgtatt gatggaattt				340
Asp Thr Lys Asn Tyr Lys Gln Thr Ser Val				
	95	100		
ctggcttttct aaatgattttt acttttctgcc ttgaattttc aaggcataga tgtcaactta				400
cagaataaca tggttttaaga taattaagtt taaaccagag aatttgattg ttactcattt				460
tgctctcatg ttctaaacag caacagtgtg actagtcttt tgttgtaaataa gggtattttc				520
cttataagaa ttttaagaac taaaaaaaaa aaaa				554

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Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val	
gcc gcg ggc ctt ggg ccc gta atc tca cga cct ccg cct gcg gcc tcc	157
Ala Ala Gly Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser	
tcg caa aac aag ggc tcc aag cgc cgc cag ctc ttg gcc aca tta cgg	205
Ser Gln Asn Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg	
gcc cta gag gca gca tct ctt tcc cag cat ccc ccc agc cta tgt ata	253
Ala Leu Glu Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile	
agt gac tct gag gag gag gag gag gaa agg aag aag aaa tgc ccc aaa	301
Ser Asp Ser Glu Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys	
aag gca tca ttt gcc agt gcc tct gct gaa gta ggg aag aaa ggg aag	349
Lys Ala Ser Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys	
aag aaa tgt caa aaa cag ggc cca cct tgc agt gac tct gag gaa gaa	397
Lys Lys Cys Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Glu	

			75					80					85				
gta	gaa	agg	aag	aaa	tgc	cac	aaa	cag	gct	ctt	gtt	ggc	agt	gac			445
Val	Glu	Arg	Lys	Lys	Lys	Cys	His	Lys	Gln	Ala	Leu	Val	Gly	Ser	Asp		
			90					95					100				
tct	gct	gaa	gat	gag	aaa	aga	aag	agg	aaa	tgc	cag	aaa	cat	gcc	cct		493
Ser	Ala	Glu	Asp	Glu	Lys	Arg	Lys	Arg	Lys	Cys	Gln	Lys	His	Ala	Pro		
			105					110					115				
ata	aat	tca	gcc	cag	cac	ctg	gac	aat	gtt	gac	caa	aca	ggg	ccc	aaa		541
Ile	Asn	Ser	Ala	Gln	His	Leu	Asp	Asn	Val	Asp	Gln	Thr	Gly	Pro	Lys		
			120			125				130					135		
gcc	tgg	aag	ggg	agt	act	aca	aat	gat	cca	cca	aag	caa	agc	cct	ggg		589
Ala	Trp	Lys	Gly	Ser	Thr	Thr	Asn	Asp	Pro	Pro	Lys	Gln	Ser	Pro	Gly		
					140				145					150			
tcc	act	tcc	cct	aaa	ccc	cct	cat	aca	tta	agc	cgc	aag	cag	tgg	cgg		637
Ser	Thr	Ser	Pro	Lys	Pro	Pro	His	Thr	Leu	Ser	Arg	Lys	Gln	Trp	Arg		
			155					160					165				
aac	cgg	caa	aag	aat	aag	aga	aga	tgt	aag	aac	aag	ttt	cag	cca	cct		685
Asn	Arg	Gln	Lys	Asn	Lys	Arg	Arg	Cys	Lys	Asn	Lys	Phe	Gln	Pro	Pro		
			170					175					180				
cag	gtg	cca	gac	cag	gcc	cca	gct	gag	gcc	ccc	aca	gag	aag	aca	gag		733
Gln	Val	Pro	Asp	Gln	Ala	Pro	Ala	Glu	Ala	Pro	Thr	Glu	Lys	Thr	Glu		
			185				190				195						
gtg	tct	cct	gtt	ccc	agg	aca	gac	agc	cat	ggg	gct	cgg	gca	ggg	gct		781
Val	Ser	Pro	Val	Pro	Arg	Thr	Asp	Ser	His	Gly	Ala	Arg	Ala	Gly	Ala		
			200				205				210				215		
ttg	cga	gcc	cgc	atg	gca	cag	cgg	ctg	gat	ggg	gcc	cga	ttt	cgc	tac		829
Leu	Arg	Ala	Arg	Met	Ala	Gln	Arg	Leu	Asp	Gly	Ala	Arg	Phe	Arg	Tyr		
					220				225					230			
ctc	aat	gaa	cag	ttg	tac	tca	ggg	ccc	agc	agt	gct	gca	cag	cgt	ctc		877
Leu	Asn	Glu	Gln	Leu	Tyr	Ser	Gly	Pro	Ser	Ser	Ala	Ala	Gln	Arg	Leu		
			235					240					245				
ttc	cag	gaa	gac	cct	gag	gct	ttt	ctt	ctc	tac	cac	cgc	ggc	ttc	cag		925
Phe	Gln	Glu	Asp	Pro	Glu	Ala	Phe	Leu	Leu	Tyr	His	Arg	Gly	Phe	Gln		
			250				255					260					
agc	caa	gtg	aag	aag	tgg	cca	ctg	cag	cca	gtg	gac	cgc	atc	gcc	agg		973
Ser	Gln	Val	Lys	Lys	Trp	Pro	Leu	Gln	Pro	Val	Asp	Arg	Ile	Ala	Arg		
			265				270					275					
gat	ctt	cgc	cag	cgg	cct	gca	tcc	cta	gtg	gtg	gct	gac	ttc	ggc	tgt		1021
Asp	Leu	Arg	Gln	Arg	Pro	Ala	Ser	Leu	Val	Val	Ala	Asp	Phe	Gly	Cys		
			280			285				290					295		
ggg	gat	tgc	cgc	ttg	gct	tca	agt	atc	cgg	aac	cct	gtg	cat	tgc	ttt		1069
Gly	Asp	Cys	Arg	Leu	Ala	Ser	Ser	Ile	Arg	Asn	Pro	Val	His	Cys	Phe		
					300				305					310			
gac	ttg	gct	tct	ctg	gac	cct	agg	gtc	act	gtg	tgt	gac	atg	gcc	cag		1117
Asp	Leu	Ala	Ser	Leu	Asp	Pro	Arg	Val	Thr	Val	Cys	Asp	Met	Ala	Gln		
			315					320					325				
gtt	cct	ttg	gag	gat	gag	tct	gtg	gat	gtg	gct	gtg	ttt	tgc	ctt	tca		1165
Val	Pro	Leu	Glu	Asp	Glu	Ser	Val	Asp	Val	Ala	Val	Phe	Cys	Leu	Ser		
			330				335					340					
ctg	atg	gga	acc	aac	atc	agg	gac	ttc	cta	gag	gag	gca	aat	aga	gta		1213
Leu	Met	Gly	Thr	Asn	Ile	Arg	Asp	Phe	Leu	Glu	Glu	Ala	Asn	Arg	Val		
			345			350					355						
ctg	aag	cca	ggg	ggg	ctc	ctg	aaa	gtg	gct	gag	gtc	agc	agc	cgc	ttt		1261
Leu	Lys	Pro	Gly	Gly	Leu	Leu	Lys	Val	Ala	Glu	Val	Ser	Ser	Arg	Phe		
			360			365				370					375		
gag	gat	gtt	cga	acc	ttt	ctg	cgg	gct	gtg	acc	aag	cta	ggc	ttc	aag		1309
Glu	Asp	Val	Arg	Thr	Phe	Leu	Arg	Ala	Val	Thr	Lys	Leu	Gly	Phe	Lys		

	380	385	390	
att gtc tcc aag gac ctg acc aac agc cat ttc ttc ttg ttt gat ttc				1357
Ile Val Ser Lys Asp Leu Thr Asn Ser His Phe Phe Leu Phe Asp Phe				
	395	400	405	
caa aag act ggg ccc cct ctg gta ggg ccc aag gct cag ctt tca ggc				1405
Gln Lys Thr Gly Pro Pro Leu Val Gly Pro Lys Ala Gln Leu Ser Gly				
	410	415	420	
ctg cag ctt cag cca tgt ctc tac aag cgc agg tgacctctgg atcttccttg				1458
Leu Gln Leu Gln Pro Cys Leu Tyr Lys Arg Arg				
	425	430		
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tgtgagccaa gacctgggtc ctggtggacc ctgaggacaa agtgtgataa aacctctggc				1578
tcagacttgc tctactgaag gcttcttggt tataaatgac ataaagtcac tggggctagc				1638
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 <223> Von Heijne matrix
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 <221> polyA_signal
 <222> 452..457
 <221> polyA_site
 <222> 482..494
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cag ttt ttc ttg aga att gat ggg gtg ctt atc aga atg aat gac acg	99
Gln Phe Phe Leu Arg Ile Asp Gly Val Leu Ile Arg Met Asn Asp Thr	
-5 1 5	
aga ctt tac cat gag gct gac aag acc tac atg tta cga gaa tat acg	147
Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr Met Leu Arg Glu Tyr Thr	
10 15 20	
tca cga gaa agc aaa att tct agt ttg atg cat gtt cca cct tcc ctc	195
Ser Arg Glu Ser Lys Ile Ser Ser Leu Met His Val Pro Pro Ser Leu	
25 30 35 40	
ttc acg gaa cct aat gaa ata tcc cag tat tta cca ata aag gaa gca	243
Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr Leu Pro Ile Lys Glu Ala	
45 50 55	
gtt tgt gag aag cta ata ttt cca gaa aga att gat cct aac cca gca	291
Val Cys Glu Lys Leu Ile Phe Pro Glu Arg Ile Asp Pro Asn Pro Ala	
60 65 70	

gac tca caa aaa agt aca caa gtg gaa taaaatgtga tacaacatat 338
Asp Ser Gln Lys Ser Thr Gln Val Glu
75 80

actcactatg gaatctgact ggacaccttg gctatattgta aggggttatt tttattatga 398
gaattaattg ccttgtttat gtacagattt tctgtagcct taaaggaaaa aaaaataaag 458
atcgttacag gcaggtttca ctcaaaaaaa aaaaac 494

<210> 109
<211> 714
<212> DNA
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<223> Von Heijne matrix
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seq PCYYLGLFQRALA/SV

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Tacccttgag tgatgtgcct tga atg acg ctg ctt tca ttc gct gct ttc acg 113
Met Thr Leu Leu Ser Phe Ala Ala Phe Thr
-25 -20

gct gct ttc tcc gtc ctc ccc tgt tac tac ctt ggg ctg ttt cag cgg 161
Ala Ala Phe Ser Val Leu Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg
-15 -10 -5

gcg ctc gcg tcg gtc ttc gac cca ctt tgc gtt tgt tca cgt gtg ctc 209
Ala Leu Ala Ser Val Phe Asp Pro Leu Cys Val Cys Ser Arg Val Leu
1 5 10

ccg aca cct gta tgt acc ttg gtc gca aca caa gcc gaa aaa ata tta 257
Pro Thr Pro Val Cys Thr Leu Val Ala Thr Gln Ala Glu Lys Ile Leu
15 20 25

gag aat ggg ccc tgt cca acc aag gag gcg gcc cag ctt gtc ggg aag 305
Glu Asn Gly Pro Cys Pro Thr Lys Glu Ala Ala Gln Leu Val Gly Lys
30 35 40 45

ggc agc gtt tcc gcc aga aat gct tcg tgaaaggcac ttgagggacc 352
Gly Ser Val Ser Ala Arg Asn Ala Ser
50

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gggggtggctc atgcctgtgg tcccagcact ttgggaggcc ggggcgggcg gatcacctga 472
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aaaactagcc ggggtgtggtg gcgcatgcct gtagtcccag ctactcggga gggtagggca 592
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aa 714

<210> 110
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 <212> DNA
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<221> sig_peptide
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 <223> Von Heijne matrix
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 seq VLLLAALPPVLLP/GA

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<221> polyA_site
 <222> 793..805

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 ccc ttc ccc gtg ctc ctt ctg gcc gct ctg cct ccg gtg ctg ctg cct 100
 Pro Phe Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro
 -15 -10 -5
 ggg gcg gcc ggc ttc aca cct tcc ctc gat agc gac ttc acc ttt acc 148
 Gly Ala Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr
 1 5 10 15
 ctt ccc gcc ggc cag aag gag tgc ttc tac cag ccc atg ccc ctg aag 196
 Leu Pro Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys
 20 25 30
 gcc tcg ctg gag atc gag tac caa gtt tta gat gga gca gta tta gat 244
 Ala Ser Leu Glu Ile Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp
 35 40 45
 att gat ttc cat ctt gcc tct cca gaa ggc aaa acc tta gtt ttt gaa 292
 Ile Asp Phe His Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu
 50 55 60
 caa aga aaa tca gat gga gtt cac act gta gag act gaa gtt ggt gat 340
 Gln Arg Lys Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp
 65 70 75 80
 tac atg ttc tgc ttt gac aat aca ttc agc acc att tct gag aag gtg 388
 Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val
 85 90 95
 att ttc ttt gaa tta atc ctg gat aat atg gga gaa cag gca caa gaa 436
 Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu
 100 105 110
 caa gaa gat tgg aag aaa tat att act ggc aca gat ata ttg gat atg 484
 Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp Met
 115 120 125
 aaa ctg gaa gac atc ctg gaa tcc atc agc agc atc aag tcc aga cta 532
 Lys Leu Glu Asp Ile Leu Glu Ser Ile Ser Ser Ile Lys Ser Arg Leu
 130 135 140
 agc aaa agt ggg cac ata caa att ctg ctt aga gca ttt gaa gct cgt 580
 Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe Glu Ala Arg

145	150	155	160	
gat cga aac ata caa gaa agc aac ttt gat aga gtc aat ttc tgg tct				628
Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val Asn Phe Trp Ser				
	165	170	175	
atg gtt aat tta gtg gtc atg gtg gtg gtg tca gcc att caa gtt tat				676
Met Val Asn Leu Val Val Met Val Val Val Ser Ala Ile Gln Val Tyr				
	180	185	190	
atg ctg aag agt ctg ttt gaa gat aag agg aaa agt aga act				718
Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr				
	195	200	205	
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ttacagtcaa gaccaaaaaa aaaaaaa				805

<210> 111

<211> 787

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> 26..88

<223> Von Heijne matrix

score 4.4

seq AVASSFFCASLFS/AV

<221> polyA_signal

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<221> polyA_site

<222> 775..787

<400> 111

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Val Ala Ser Ser Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys	
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ata gaa gag gga cat att ggg gta tat tac aga ggc ggt gcc ctg ctg	148
Ile Glu Glu Gly His Ile Gly Val Tyr Tyr Arg Gly Gly Ala Leu Leu	
5 10 15 20	
act tcg acc agc ggc cct ggt ttc cat ctc atg ctc cct ttc atc aca	196
Thr Ser Thr Ser Gly Pro Gly Phe His Leu Met Leu Pro Phe Ile Thr	
25 30 35	
tca tat aag tct gtg cag acc aca ctc cag aca gat gag gtg aag aat	244
Ser Tyr Lys Ser Val Gln Thr Thr Leu Gln Thr Asp Glu Val Lys Asn	
40 45 50	
gta cct tgt ggg act agt ggt ggt gtg atg atc tac ttt gac aga att	292
Val Pro Cys Gly Thr Ser Gly Gly Val Met Ile Tyr Phe Asp Arg Ile	
55 60 65	
gaa gtg gtg aac ttc ctg gtc ccg aac gca gtg cat gat ata gtg aag	340
Glu Val Val Asn Phe Leu Val Pro Asn Ala Val His Asp Ile Val Lys	

70	75	80	
aac tat act gct gac tat gac aag gcc ctc atc ttc aac aag atc cac			388
Asn Tyr Thr Ala Asp Tyr Asp Lys Ala Leu Ile Phe Asn Lys Ile His			
85	90	95	100
cac gaa ctg aac cag ttc tgc agt gtg cac acg ctt caa gag gtc tac			436
His Glu Leu Asn Gln Phe Cys Ser Val His Thr Leu Gln Glu Val Tyr			
105	110	115	
att gag ctg ttt gga ctg gaa aat gat ttt tcc cag gaa tct tca			481
Ile Glu Leu Phe Gly Leu Glu Asn Asp Phe Ser Gln Glu Ser Ser			
120	125	130	
taaaagggac cctgagcaag aacatttttc atagcagaca ggaggactca tccacatcgc			541
cagcaatcat aattaagcaa accgcctttt gcaccattta agatttagga aatcatccaa			601
attactttta atgtttctgc agtagaaaat gaatctaaat tcattttata gggttttag			661
tcttttatct gttttggatt cactgtgctt ttaagaaaaa gttggtaaat ttgccgttga			721
tttttctttt taacctcaaaa ctaatagaat tttataaaat attaattttc tccaaaaaaa			781
aaaaaa			787

<210> 112

<211> 569

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26..562

<221> sig_peptide

<222> 26..187

<223> Von Heijne matrix

score 4.1

seq AVVAAAAARTGSEA/RV

<400> 112

ggaacaggt ctgggctaca aaagt atg gcc gct tct gag gcg gcg gtg gtg	52
Met Ala Ala Ser Glu Ala Ala Val Val	
-50	
tct tcg ccg tct ttg aaa aca gac aca tcc cct gtc ctt gaa act gca	100
Ser Ser Pro Ser Leu Lys Thr Asp Thr Ser Pro Val Leu Glu Thr Ala	
-45 -40 -35 -30	
gga acg gtc gca gca atg gct gcg acc ccg tca gca agg gct gca gcc	148
Gly Thr Val Ala Ala Met Ala Ala Thr Pro Ser Ala Arg Ala Ala Ala	
-25 -20 -15	
gcg gtg gtt gcg gcc gcg gcc agg acc gga tcc gaa gcc agg gtc tcc	196
Ala Val Val Ala Ala Ala Ala Arg Thr Gly Ser Glu Ala Arg Val Ser	
-10 -5 1	
aag gcc gct ttg gct acc aag ctg ctg tcc ttg agc ggc gtg ttc gcc	244
Lys Ala Ala Leu Ala Thr Lys Leu Leu Ser Leu Ser Gly Val Phe Ala	
5 10 15	
gtg cac aag ccc aaa ggg ccc act tca gcc gag ctg ctg aat cgg ttg	292
Val His Lys Pro Lys Gly Pro Thr Ser Ala Glu Leu Leu Asn Arg Leu	
20 25 30 35	
aag gag aag ctg ctg gca gaa gct gga atg cct tct cca gaa tgg acc	340
Lys Glu Lys Leu Leu Ala Glu Ala Gly Met Pro Ser Pro Glu Trp Thr	
40 45 50	
aag agg aaa aag cag act ttg aaa att ggg cat gga ggg act cta gac	388

Lys	Arg	Lys	Lys	Gln	Thr	Leu	Lys	Ile	Gly	His	Gly	Gly	Thr	Leu	Asp	
			55					60					65			
agc	gca	gcc	cga	gga	gtt	ctg	gtt	gtt	gga	att	gga	agc	gga	aca	aaa	436
Ser	Ala	Ala	Arg	Gly	Val	Leu	Val	Val	Gly	Ile	Gly	Ser	Gly	Thr	Lys	
		70					75					80				
atg	ttg	acc	agt	atg	ttg	tca	ggg	tcc	aag	agg	tat	act	gcc	att	gga	484
Met	Leu	Thr	Ser	Met	Leu	Ser	Gly	Ser	Lys	Arg	Tyr	Thr	Ala	Ile	Gly	
	85					90				95						
gaa	ctg	ggg	aaa	gct	act	gat	aca	cta	gat	tct	acg	ggg	aag	gta	aca	532
Glu	Leu	Gly	Lys	Ala	Thr	Asp	Thr	Leu	Asp	Ser	Thr	Gly	Lys	Val	Thr	
100					105					110					115	
gaa	gaa	aaa	cct	tac	ggg	atg	aac	ctc	atc	taagtag						569
Glu	Glu	Lys	Pro	Tyr	Gly	Met	Asn	Leu	Ile							
			120						125							

<210> 113

<211> 893

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..810

<221> sig_peptide

<222> 4..279

<223> Von Heijne matrix

score 6.8

seq AVMLYTWRSCSRA/IP

<221> polyA_signal

<222> 858..863

<221> polyA_site

<222> 881..893

<400> 113

gcc	atg	atc	acg	cac	gtc	acc	ctg	gaa	gat	gcc	ctg	tcc	aac	gtg	gac	48
Met	Ile	Thr	His	Val	Thr	Leu	Glu	Asp	Ala	Leu	Ser	Asn	Val	Asp		
		-90					-85				-80					
ctg	ctt	gaa	gag	ctt	ccc	ctc	ccc	gac	cag	cag	cca	tgc	atc	gag	cct	96
Leu	Leu	Glu	Glu	Leu	Pro	Leu	Pro	Asp	Gln	Gln	Pro	Cys	Ile	Glu	Pro	
	-75					-70					-65					
cca	cct	tcc	tcc	atc	atg	tac	cag	gct	aac	ttt	gac	aca	aac	ttt	gag	144
Pro	Pro	Ser	Ser	Ile	Met	Tyr	Gln	Ala	Asn	Phe	Asp	Thr	Asn	Phe	Glu	
	-60				-55					-50						
gac	agg	aat	gca	ttt	gtc	acg	ggc	att	gca	agg	tac	att	gag	cag	gct	192
Asp	Arg	Asn	Ala	Phe	Val	Thr	Gly	Ile	Ala	Arg	Tyr	Ile	Glu	Gln	Ala	
	-45			-40			-35				-30					
aca	gtc	cac	tcc	agc	atg	aat	gag	atg	ctg	gag	gaa	gga	cat	gag	tat	240
Thr	Val	His	Ser	Ser	Met	Asn	Glu	Met	Leu	Glu	Glu	Gly	His	Glu	Tyr	
			-25				-20				-15					
gcg	gtc	atg	ctg	tac	acc	tgg	cgc	agc	tgt	tcc	cgg	gcc	att	ccc	cag	288
Ala	Val	Met	Leu	Tyr	Thr	Trp	Arg	Ser	Cys	Ser	Arg	Ala	Ile	Pro	Gln	
		-10					-5					1				

gtg aaa tgc aac gag cag ccc aac cga gta gag atc tat gag aag aca	336
Val Lys Cys Asn Glu Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr	
5 10 15	
gta gag gtg ctg gag ccg gag gtc acc aag ctc atg aag ttc atg tat	384
Val Glu Val Leu Glu Pro Glu Val Thr Lys Leu Met Lys Phe Met Tyr	
20 25 30 35	
ttt cag cgc aag gcc atc gag cgg ttc tgc agc gag gtg aag cgg ctg	432
Phe Gln Arg Lys Ala Ile Glu Arg Phe Cys Ser Glu Val Lys Arg Leu	
40 45 50	
tgc cat gcc gag cgc agg aag gac ttt gtc tct gag gcc tac ctc ctg	480
Cys His Ala Glu Arg Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Leu	
55 60 65	
acc ctt ggc aag ttc atc aac atg ttt gct gtc ctg gat gag cta aag	528
Thr Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys	
70 75 80	
aac atg aag tgc agc gtc aag aat gac cac tcc gcc tac aag agg gca	576
Asn Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala	
85 90 95	
gca cag ttc ctg cgg aag atg gca gat ccc cag tct atc cag gag tcg	624
Ala Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser	
100 105 110 115	
cag aac ctt tcc atg ttc ctg gcc aac cac aac agg atc acc cag tgt	672
Gln Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys	
120 125 130	
ctc cac cag caa ctt gaa gtg atc cca ggc tat gag gag ctg ctg gct	720
Leu His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala	
135 140 145	
gac att gtc aac atc tgt gtg gat tac tac gag aac aag atg tac ctg	768
Asp Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu	
150 155 160	
act ccc agt gag aaa cat atg ctc ctc aag gta aaa ctc ccc	810
Thr Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro	
165 170 175	
tgaggccgca cccatggagc ctgggcttac cctctcacct tcttcttatt aaaaatccgt	870
ttttaaaaaaac aaaaaaaaaaaa aaa	893

<210> 114

<211> 1475

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 55..459

<221> sig_peptide

<222> 55..120

<223> Von Heijne matrix

score 7.2

seq GLWLALVDGLVRS/SP

<221> polyA_signal

<222> 1444..1449

<221> polyA_site

<222> 1462..1475

<400> 114

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cagttccgca gctacgtgtg ggacccgctg ctgacccctgt cgcagatcgt cctc atg      57
                                   Met
cag acc gtg tat tac ggc tcg ctg ggc ctg tgg ctg gcg ctg gtg gac      105
Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp
   -20               -15               -10
ggg cta gtg cga agc agc ccc tcg ctg gac cag atg ttc gac gcc gag      153
Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala Glu
   -5               1               5               10
atc ctg ggc ttt tcc acc cct cca ggc cgg ctc tcc atg atg tcc ttc      201
Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe
               15               20               25
atc ttc aac gcc ctc acc tgt gcc ctg ggc ttg ctg tac ttc atc cgg      249
Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg
               30               35               40
cga gga aag cag tgt ctg gat ttc act gtc act gtc cat ttc ttt cac      297
Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His
   45               50               55
ctc ctg ggc tgc tgg ttc tac agc tcc cgt ttc ccc tcg gcg ctg acc      345
Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr
   60               65               70               75
tgg tgg ctg gtc caa gcc gtg tgc att gca ctc atg gct gtc atc ggg      393
Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly
               80               85               90
gag tac ctg tgc atg cgg acg gag ctc aag gag ata ccc ctc aac tca      441
Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn Ser
               95               100               105
gcc cct aaa tcc aat gtc tagaatcagg ccctttggac atcccgtga      489
Ala Pro Lys Ser Asn Val
               110
cacttggggcc ccttaacacc ttgggctgct cagaccctcc agatgaggtc cagcccagat      549
ctgagaggaa ccctggaaat gtgaagtctc tgttggtgtg ggagagatag tgagggcctg      609
tcaaagaagg caggtagcag tcagcatgac agctgcaaga atgacctctg tctgttgaag      669
cccttggtatc tgagaggcca ggaaggggac ctctttgagg gtaataacat aattggaacc      729
atgccactct tgagccacaa tacctgtcac cagcctgttg ttttaagaga gaaaaaaaaat      789
caaggatatac tgattggagc aaaccacttc tttagtcac tgtcttacct ccctgggaca      849
gctgttacct ttgcagtgtt gccgaatcac agcagttacc tttgcaatgt tgccgaatca      909
cagcagttct gttggagaaa cgcttggttt cggatccag agccacagaa agaaatgtag      969
gtgtgaagta ttaggctgct gtcagggaga ggatggcaga tggaggcatc aagcacaagg      1029
aaaatgcaca acctgtgccc tggtatacac acgttcatgt gcgccaaga acctatgact      1089
ttcttccagt tccttctacc aggtcccat cctgtgcca gctctcaaca tagcaggcca      1149
taggaccag agaagaatcc cagtgttgct caaagtctga ccatcataaa gacactgcct      1209
gtcttctagg aatgaccagg caccagctc ccactggact ccaatttttt ttcctgcctt      1269
attagaatt ctttggcggg aagggtatga tgggttcca gagacaagaa gcccaacctt      1329
ctggcctggg ctgtgctgat agtgctgagg gagataggaa tttgctgcta agatttttct      1389
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gtattttcca tgaaaaaaaaa aaaaaa      1475

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<210> 115

<211> 321

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 48..248

<221> sig_peptide
 <222> 48..161
 <223> Von Heijne matrix
 score 6.3
 seq LVFALVTAVCCCLA/DG

<221> polyA_signal
 <222> 283..288

<221> polyA_site
 <222> 308..321

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<400> 115
gctgagaaga gttgagggaa agtgctgctg ctgggtctgc agacgcg atg aat aac      56
                                     Met Asn Asn
gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc      104
Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly
-35          -30          -25          -20
cac gtg aag atg ctg cgg ctg gtg ttt gca ctt gtg aca gca gta tgc      152
His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr Ala Val Cys
          -15          -10          -5
tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc      200
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro
          1          5          10
aac ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      248
Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
          15          20          25
tgattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      308
aaaaaaaaaa aaa      321

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<210> 116
 <211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..399

<221> sig_peptide
 <222> 25..186
 <223> Von Heijne matrix
 score 3.5
 seq SILAQVLDQSARA/RL

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<400> 116
ctgctccagc gctgacgccg agcc atg gcg gac gag gag ctt gag gcg ctg      51
                                     Met Ala Asp Glu Glu Leu Glu Ala Leu
                                     -50
agg aga cag agg ctg gcc gag ctg cag gcc aaa cac ggg gat cct ggt      99
Arg Arg Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly

```

-45	-40	-35	-30	
gat gcg gcc caa cag gaa gca aag cac agg gaa gca gaa atg aga aac				147
Asp Ala Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn				
	-25	-20	-15	
agt atc tta gcc caa gtt ctg gat cag tcg gcc cgg gcc agg tta agt				195
Ser Ile Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser				
	-10	-5	1	
aac tta gca ctt gta aag cct gaa aaa act aaa gca gta gag aat tac				243
Asn Leu Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr				
5	10	15		
ctt ata cag atg gca aga tat gga caa cta agt gag aag gta tca gaa				291
Leu Ile Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu				
20	25	30	35	
caa ggt tta ata gaa atc ctt aaa aaa gta agc caa caa aca gaa aag				339
Gln Gly Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys				
	40	45	50	
aca aca aca gtg aaa ttc aac aga aga aaa gta atg gac tct gat gaa				387
Thr Thr Thr Val Lys Phe Asn Arg Arg Lys Val Met Asp Ser Asp Glu				
	55	60	65	
gat gac gat tat tgaactacaa gtgctcacag actagaactt aacggaacaa				439
Asp Asp Asp Tyr				
70				
gtctaggaca g				450

<210> 117
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..1137
 <221> sig_peptide
 <222> 10..72
 <223> Von Heijne matrix
 score 6.5
 seq LLTLLLPPPPPLYT/RH

<221> polyA_signal
 <222> 1144..1149

<221> polyA_site
 <222> 1162..1173

<400> 117	
gagctgctt atg gga cac cgc ttc ctg cgc ggc ctc tta acg ctg ctg ctg	51
Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu	
	-20
ccg ccg cca ccc ctg tat acc cgg cac cgc atg ctc ggt cca gag tcc	99
Pro Pro Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser	
	-5
gtc ccg ccc cca aaa cga tcc cgc agc aaa ctc atg gca ccg ccc cga	147
Val Pro Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg	
10	15
	20
	25

atc ggg acg cac aat ggc acc ttc cac tgc gac gag gca ctg gca tgc	195
Ile Gly Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys	
30 35 40	
gca ctg ctt cgc ctc ctg ccg gag tac cgg gat gca gag att gtg cgg	243
Ala Leu Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg	
45 50 55	
acc cgg gat ccc gaa aaa ctc gct tcc tgt gac atc gtg gtg gac gtg	291
Thr Arg Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val	
60 65 70	
ggg ggc gag tac gac cct cgg aga cac cga tat gac cat cac cag agg	339
Gly Gly Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg	
75 80 85	
tct ttc aca gag acc atg agc tcc ctg tcc cct ggg agg ccg tgg cag	387
Ser Phe Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln	
90 95 100 105	
acc aag ctg agc agt gcg gga ctc atc tat ctg cac ttc ggg cac aag	435
Thr Lys Leu Ser Ser Ala Gly Leu Ile Tyr Leu His Phe Gly His Lys	
110 115 120	
ctg ctg gcc cag ttg ctg ggc act agt gaa gag gac agc atg gtg ggc	483
Leu Leu Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly	
125 130 135	
acc ctc tat gac aag atg tat gag aac ttt gtg gag gag gtg gat gct	531
Thr Leu Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Glu Val Asp Ala	
140 145 150	
gtg gac aat ggg atc tcc cag tgg gca gag ggg gag cct cga tat gca	579
Val Asp Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala	
155 160 165	
ctg acc act acc ctg agt gca cga gtt gct cga ctt aat cct acc tgg	627
Leu Thr Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp	
170 175 180 185	
aac cac ccc gac caa gac act gag gca ggg ttc aag cgt gca atg gat	675
Asn His Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp	
190 195 200	
ctg gtt caa gag gag ttt ctg cag aga tta gat ttc tac caa cac agc	723
Leu Val Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser	
205 210 215	
ggg ctg cca gcc cgg gcc ttg gtg gaa gag gcc ctt gcc cag cga ttc	771
Trp Leu Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe	
220 225 230	
cag gtg gac cca agt gga gag att gtg gaa ctg gcg aaa ggt gca tgt	819
Gln Val Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys	
235 240 245	
ccc tgg aag gag cat ctc tac cac ctg gaa tct ggg ctg tcc cct cca	867
Pro Trp Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro	
250 255 260 265	
gtg gcc atc ttc ttt gtt atc tac act gac cag gct gga cag tgg cga	915
Val Ala Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg	
270 275 280	
ata cag tgt gtg ccc aag gag ccc cac tca ttc caa agc cgg ctg ccc	963
Ile Gln Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro	
285 290 295	
ctg cca gag cca tgg cgg ggt ctt cgg gac gag gcc ctg gac cag gtc	1011
Leu Pro Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val	
300 305 310	
agt ggg atc cct ggc tgc atc ttc gtc cat gca agc ggc ttc att ggc	1059
Ser Gly Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly	
315 320 325	


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ggt cac cgc acc cga gag ggt gcc ttg agc atg gcc cgt gcc acc ttg 1107
Gly His Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu
330          335          340          345
gcc cag cgc tca tac ctc cca caa atc tcc tagtctaata aaaccttcca 1157
Ala Gln Arg Ser Tyr Leu Pro Gln Ile Ser
          350          355
tctcaaaaaa aaaaaa 1173

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<210> 118
 <211> 785
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 72..704

<221> sig_peptide
 <222> 72..161
 <223> Von Heijne matrix
 score 13.2
 seq LLLLSTLVIPSAA/AP

<221> polyA_signal
 <222> 772..777

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400> 118
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aggggacgggg t atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat 110
          Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His
          -30          -25          -20
ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct 158
Leu Leu Val Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala
          -15          -10          -5
gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc 206
Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu
          1          5          10          15
aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa 254
Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys
          20          25          30
ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac 302
Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp
          35          40          45
ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag cac 350
Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His
          50          55          60
cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag gta 398
Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val
          65          70          75
ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg 446
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr
          80          85          90          95
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att 494
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile
          100          105          110

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aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac      542
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His
      115                      120                      125
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc      590
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu
      130                      135                      140
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc      638
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser
      145                      150                      155
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc      686
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu
      160                      165                      170                      175
agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg      734
Arg Pro Ser Arg Gln Leu
      180
tagcccccat cagaccctgc cccaagcacc atatggaaat aaagttcttt c      785

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<210> 119

<211> 559

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 44..505

<221> sig_peptide

<222> 44..223

<223> Von Heijne matrix

score 4

seq LVRRTLLVAALRA/WM

<400> 119

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mgcaaccaga gggagatgat cacctgaacc actgctccaa acc atg ggc agt aaa      55
Met Gly Ser Lys
      -60
tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag agg cgg      103
Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln Arg Arg
      -55                      -50                      -45
cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg aag gca      151
Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val Lys Ala
      -40                      -35                      -30                      -25
gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc agg acc      199
Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg Arg Thr
      -20                      -15                      -10
ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg tgg agg      247
Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp Trp Arg
      -5                      1                      5
acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg ttg agg      295
Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu Leu Arg
      10                      15                      20
gtc tac gtc atc cag gag cag gcg acg gtc aag ctc cag tcc tgc atc      343
Val Tyr Val Ile Gln Glu Ala Thr Val Lys Leu Gln Ser Cys Ile
      25                      30                      35                      40
cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat gct ctc      391

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Arg	Met	Trp	Gln	Cys	Arg	Gln	Cys	Tyr	Arg	Gln	Met	Cys	Asn	Ala	Leu		
			45					50					55				
tgc	ttg	ttc	cag	gtc	cca	gag	agc	agc	ctt	gcc	ttc	cag	act	gat	ggc	439	
Cys	Leu	Phe	Gln	Val	Pro	Glu	Ser	Ser	Leu	Ala	Phe	Gln	Thr	Asp	Gly		
			60					65					70				
ttt	tta	cag	gtc	caa	tat	gca	atc	cct	tca	aag	cag	cca	gag	ttc	cac	487	
Phe	Leu	Gln	Val	Gln	Tyr	Ala	Ile	Pro	Ser	Lys	Gln	Pro	Glu	Phe	His		
			75					80					85				
att	gaa	atc	cta	tca	atc	tgaaaggcct	ggggcatgga	gaacaggctg								535	
Ile	Glu	Ile	Leu	Ser	Ile												
			90														
cactacccta	ataaatgtct	gacc														559	

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 <213> Homo sapiens

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 <221> sig_peptide
 <222> 25..150
 <223> Von Heijne matrix
 score 4.6
 seq LDPAVSLSAPAFA/SA
 <221> polyA_signal
 <222> 734..739
 <221> polyA_site
 <222> 757..770

<400> 120																	
cgagaaaagg	agagacacac	atac	atg	aaa	gga	gga	gct	ttc	tcc	aat	ctt					51	
			Met	Lys	Gly	Gly	Ala	Phe	Ser	Asn	Leu						
			-40				-35										
aat	gat	tcc	cag	ctc	tca	gcc	tcg	ttt	ctg	caa	ccc	agc	ctg	caa	gca	99	
Asn	Asp	Ser	Gln	Leu	Ser	Ala	Ser	Phe	Leu	Gln	Pro	Ser	Leu	Gln	Ala		
			-30				-25					-20					
aac	tgt	cct	gct	ttg	gac	cct	gct	gtg	tca	ctc	tcc	gca	cca	gcc	ttt	147	
Asn	Cys	Pro	Ala	Leu	Asp	Pro	Ala	Val	Ser	Leu	Ser	Ala	Pro	Ala	Phe		
			-15				-10					-5					
gcc	tct	gct	ctt	cgc	tct	atg	aag	tcc	tcc	cag	gct	gca	cgg	aag	gac	195	
Ala	Ser	Ala	Leu	Arg	Ser	Met	Lys	Ser	Ser	Gln	Ala	Ala	Arg	Lys	Asp		
			1			5				10				15			
gac	ttt	ctc	agg	tct	ctt	agt	gat	gga	gac	tca	ggg	aca	tca	gaa	cac	243	
Asp	Phe	Leu	Arg	Ser	Leu	Ser	Asp	Gly	Asp	Ser	Gly	Thr	Ser	Glu	His		
			20				25					30					
atc	tca	gcg	gtg	gtg	act	agc	cct	cgg	att	tcc	tgc	cat	ggg	gct	gcc	291	
Ile	Ser	Ala	Val	Thr	Ser	Pro	Arg	Ile	Ser	Cys	His	Gly	Ala	Ala			
			35				40					45					
att	ccc	acc	gcc	cgt	gcc	ctc	tgc	cta	ggc	tgt	tcc	tgc	tgc	acc	gaa	339	
Ile	Pro	Thr	Ala	Arg	Ala	Leu	Cys	Leu	Gly	Cys	Ser	Cys	Cys	Thr	Glu		

50	55	60	
cgc ctc ctc ctg cca ccg ccc tcc ctc ctt tct tta gaa gcc cct gcc			387
Arg Leu Leu Leu Pro Pro Pro Ser Leu Leu Ser Leu Glu Ala Pro Ala			
65	70	75	
agc acc tgagctctct gctgattgct gttcctccca gtctgtggaa gctttgcca			443
Ser Thr			
80			
tatgctttcc ttaaaagggt tctgggcagg gcaggcgccc ccattttctca gggatcccct			503
ccaggacaac gccttttcct tgtgtcttca gctctcctta ccagatatct atatatttgt			563
atatattcag tttcaccaac aatgcatcaa gtactttttt ttttaagtaa agaaccgcag			623
tcatcgaaact ggagcccat tgattccctc cccctcgct ccccaaactt ggcacctgcc			683
caaggatatcc tcagaaccat ttgggtgtc ctttggcatt ggataataga aataaaattt			743
tacctctttc tacaaaaaaa aaaaaaac			770

<210> 121
 <211> 1213
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 58..1095
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 <222> 58..114
 <223> Von Heijne matrix
 score 5.4
 seq LSHLLPSLRQVIQ/EP

<221> polyA_site
 <222> 1202..1213

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ccttggtttt cctttgccct gctgtgtgat cttagctccc tgcccaggcc cacagcc	57
atg gcc atg gcc cag aaa ctc agc cac ctc ctg ccg agt ctg cgg cag	105
Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln	
-15 -10 -5	
gtc atc cag gag cct cag cta tct ctg cag cca gag cct gtc ttc acg	153
Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr	
1 5 10	
gtg gat cga gct gag gtg ccg ccg ctc ttc tgg aag ccg tac atc tat	201
Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr	
15 20 25	
gcg ggc tac cgg ccg ctg cat cag acc tgg cgc ttc tat ttc cgc acg	249
Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr	
30 35 40 45	
ctg ttc cag cag cac aac gag gcc gtg aat gtc tgg acc cac ctg ctg	297
Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu	
50 55 60	
gcg gcc ctg gta ctg ctg ctg ccg ctg gcc ctc ttt gtg gag acc gtg	345
Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val	
65 70 75	
gac ttc tgg gga gac cca cac gcc ctg ccc ctc ttc atc att gtc ctt	393
Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu	
80 85 90	

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gcc tct ttc acc tac ctc tcc ctc agt gcc ttg gct cac ctc ctg cag      441
Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln
   95                               100                               105

gcc aag tct gag ttc tgg cat tac agc ttc ttc ttc ctg gac tat gtg      489
Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
  110                               115                               120                               125

ggg gtg gcc gtg tac cag ttt ggc agt gcc ttg gca cac ttc tac tat      537
Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
                               130                               135                               140

gct atc gag ccc gcc tgg cat gcc cag gtg cag gct gtt ttt ctg ccc      585
Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
                               145                               150                               155

atg gct gcc ttt ctc gcc tgg ctt tcc tgc att ggc tcc tgc tat aac      633
Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
                               160                               165                               170

aag tac atc cag aaa cca ggc ctg ctg ggc cgc aca tgc cag gag gtg      681
Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
  175                               180                               185

ccc tcc gtc ctg gcc tac gca ctg gac att agt cct gtg gtg cat cgt      729
Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
  190                               195                               200                               205

atc ttc gtg tcc tcc gac ccc acc acg gat gat cca gct ctt ctc tac      777
Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
                               210                               215                               220

cac aag tgc cag gtg gtc ttc ttt ctg ctg gct gct gcc ttc ttc tct      825
His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
                               225                               230                               235

acc ttc atg ccc gag cgc tgg ttc cct ggc agc tgc cat gtc ttc ggg      873
Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
  240                               245                               250

cag ggc cac caa ctt ttc cat atc ttc ttg gtg ctg tgc acg ctg gct      921
Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
  255                               260                               265

cag ctg gag gct gtg gca ctg gac tat gag gcc cga cgg ccc atc tat      969
Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
  270                               275                               280                               285

gag cct ctg cac acg cac tgg cct cac aac ttt tct ggc ctc ttc ctg     1017
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
                               290                               295                               300

ctc acg gtg ggc agc agc atc ctc act gca ttc ctc ctg agc cag ctg     1065
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
                               305                               310                               315

gta cag cgc aaa ctt gat cag aag acc aag tgaaggggga tggcatctgg     1115
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
  320                               325

tagggaggga ggtatagttg ggggacaggg gtctggggttt ggctccaagt gggaacaagg     1175
cctggtaaag ttgtttgtgt ctggccaaaa aaaaaaaaaa     1213

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<210> 122

<211> 1318

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..660

<221> sig_peptide

<222> 31..90

<223> Von Heijne matrix

score 5.4

seq AFVIACVLSLIST/IY

<221> polyA_signal

<222> 1288..1293

<221> polyA_site

<222> 1307..1318

<400> 122

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                               Met Asp Asn Arg Phe Ala Thr Ala
                               -20                               -15
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
                               -10                               -5                               1
gct tcc att ggc aca gac ttc tgg tat gag tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
                               5                               10                               15                               20
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
                               25                               30                               35
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
                               40                               45                               50
ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met
                               55                               60                               65
cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr
                               70                               75                               80
aaa tgt gtg agt ttc aca cta act gag cag ttc atg gag aaa ttt gtt      390
Lys Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val
                               85                               90                               95                               100
gat ccc gga aac cac aat agc ggg att gat ctc ctt agg acc tat ctt      438
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr Leu
                               105                               110                               115
tgg cgt tgc cag ttc ctt tta cct ttt gtg agt tta ggt ttg atg tgc      486
Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu Met Cys
                               120                               125                               130
ttt ggg gct ttg atc gga ctt tgt gct tgc att tgc cga agc tta tat      534
Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg Ser Leu Tyr
                               135                               140                               145
ccc acc att gcc acg ggc att ctc cat ctc ctt gca gtg aca aag gag      582
Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala Val Thr Lys Glu
                               150                               155                               160
agc atg ctt cca gct gga gct gag tcc aag cac aca gcc act cct gca      630
Ser Met Leu Pro Ala Gly Ala Glu Ser Lys His Thr Ala Thr Pro Ala
                               165                               170                               175                               180
cac gca tgc gtg caa aca ggg aag ccc aag taggagaaga ggaaagaggt      680
His Ala Cys Val Gln Thr Gly Lys Pro Lys
                               185                               190

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tgtaggaggatt	tgggaagaac	cttgattatt	ccctggagga	aaagacaaat	ctacttcct	740
gaaatcacc	tcgaatctac	ttccaccctc	agaacttaaa	atgaactgca	tcctttttt	800
catcttcttt	tcttctccag	tgaatatgat	ctccaaaccc	ttattttttc	tttgaactgt	860
aaaatttcca	ctcatggacg	atgcaaccaa	cagatgcaat	ctctgagaag	atgaaaattg	920
ggacctctta	ttataaaatt	gacctagctg	gactcaggaa	accaggggaag	aagtcaatgc	980
aggcatttaa	aatgtaaagt	tttttctggt	taaatctatt	tatttttctt	gtaggttgag	1040
tatttcttcc	cagtttttct	gctctggtgt	ataacaaaca	ggtcaaaatt	tcccatcttt	1100
cctcctgata	gtagttgaat	cctaccttgc	atacttaatg	catagtgaag	tggcatctag	1160
cagaaatata	cacccccaaa	acacaccacc	atttcattag	gtgcccaaaa	aattctgtat	1220
ttagcttatt	tatttattgt	tatttttgct	ttttcttaac	ccactatata	ttgactgcaa	1280
acgaattaat	aaattatccc	ttctggaaaa	aaaaaaaa			1318

<210> 123
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..582

<221> sig_peptide
 <222> 31..90
 <223> Von Heijne matrix
 score 5.4
 seq AFVIACVLSLIST/IY

<221> polyA_signal
 <222> 816..821

<221> polyA_site
 <222> 840..853

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ggaggatggg cgagcagtct gaatgccaga atg gat aac cgt ttt gct aca gca															54
Met Asp Asn Arg Phe Ala Thr Ala															
-20 -15															
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca															102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala															
-10 -5 1															
gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa															150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln															
5 10 15 20															
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt															198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser															
25 30 35															
gat gaa gca gat gaa aag act tat aat gat gca cct ttt cga tac aat															246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Pro Phe Arg Tyr Asn															
40 45 50															
ggc aca gtg gga ttg tgg aga cgg tgt atc acc ata ccc aaa aac atg															294
Gly Thr Val Gly Leu Trp Arg Cys Ile Thr Ile Pro Lys Asn Met															
55 60 65															
cat tgg tat agc cca cca gaa agg aca gag tca ttt gat gtg gtc aca															342
His Trp Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr															
70 75 80															

[illegible]

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<210> 124
<211> 826
<212> DNA
<213> Homo sapiens

<220>
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<222> 15..695

<221> sig_peptide
<222> 15..80
<223> Von Heijne matrix
score 8.5
seq AALLLG LMMVVTG/DE

<221> polyA_signal
<222> 795..800

<221> polyA_site
<222> 814..826

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<400>	124															
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		Met	Gly	Trp	Thr	Met	Arg	Leu	Val	Thr	Ala	Ala	Leu			
				-20					-15							
tta	ctg	ggt	ctc	atg	atg	gtg	gtc	act	gga	gac	gag	gat	gag	aac	agc	98
Leu	Leu	Gly	Leu	Met	Met	Val	Val	Thr	Gly	Asp	Glu	Asp	Glu	Asn	Ser	
-10				-5						1				5		
ccg	tgt	gcc	cat	gag	gcc	ctc	ctg	gac	gag	gac	acc	ctc	ttt	tgc	cag	146
Pro	Cys	Ala	His	Glu	Ala	Leu	Leu	Asp	Glu	Asp	Thr	Leu	Phe	Cys	Gln	
			10					15					20			
ggc	ctt	gaa	gtt	ttc	tac	cca	gag	ttg	ggg	aac	att	ggc	tgc	aag	gtt	194
Gly	Leu	Glu	Val	Phe	Tyr	Pro	Glu	Leu	Gly	Asn	Ile	Gly	Cys	Lys	Val	
		25					30					35				


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gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag      242
Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
  40                               45                               50
ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg      290
Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
  55                               60                               65                               70
gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga      338
Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
                               75                               80                               85
ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag      386
Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
                               90                               95                               100
aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc      434
Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
                               105                               110                               115
cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt      482
Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
                               120                               125                               130
cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga      530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
                               135                               140                               145                               150
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa      578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
                               155                               160                               165
ccct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca      626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
                               170                               175                               180
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
                               185                               190                               195
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt      725
Gln Ala Glu Ile Ala Ala Cys
                               200                               205
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccct      785
tctttttccaa ataaaaaaaaa aatcatccaa aaaaaaaaaa a                        826

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<210> 125

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..295

<221> sig_peptide

<222> 74..196

<223> Von Heijne matrix

score 5.4

seq RLLYIGFLGYCSG/LI

<221> polyA_signal

<222> 545..550

<221> polyA_site

<222> 561..571

<400> 125

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aaacggcgctc acc atg atc gca cgg cgg aac cca gta ccc tta cgg ttt      109
                Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe
                -40                -35                -30
ctg ccg gat gag gcc cgg agc ctg ccc ccg ccc aag ctg acc gac ccg      157
Leu Pro Asp Glu Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro
                -25                -20                -15
cgg ctc ctc tac atc ggc ttc ttg ggc tac tgc tcc ggc ctg att gat      205
Arg Leu Leu Tyr Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp
                -10                -5                1
aac ctg atc cgg cgg agg ccg atc gcg acg gct ggt ttg cat cgc cag      253
Asn Leu Ile Arg Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln
                5                10                15
ctt cta tat att acg gcc ttt ttt ttg ctg gat att atc ttg      295
Leu Leu Tyr Ile Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
                20                25                30
taaaacgtga agactacctg tatgctgtga gggaccgtga aatgttttga tatatgaaat      355
tacatccaga ggatttttct gaagaagata agaaaacata tggtgaaatt tttgaaaaat      415
tccatccaat acgttgaaagt cttcaaaatg cttgctccag tttcactgat acctgctgtt      475
cctgaatttg atggaacatg tttcttatga cagttgaagc ttatgctaatt ctgtatgttg      535
cacaccttga attaaaaatac gtaccacaaaa aaaaaa      571

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<210> 126

<211> 659

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 440..658

<221> polyA_signal

<222> 601..606

<400> 126

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cgcccttacga gctgggaggt ggtgcctctc acccagctaa ttgctctcta gcccttggcc      60
ttcacagggtg ttggtgcctg ccgtgaacgc attctgacct gggccgtatc tgtctcccaa      120
gactttgtgc ctatggttgg ggacagagtg aggtcgttgc cttgacgacg acagcatgcg      180
gcccggtggc ctcctaagtg tgagcttgcg gcggaccgag gccacactgc ctccctgcct      240
gcttcgcccc ggactcgtga ctgcgtccgc agaagaaatc acaacagcgc tggaattgct      300
agtttgctag gcagcatctt ttggacctgc gaaccatatg catttcacct caaatctgtt      360
tccaagttga aaaccttttg gtctttctat gcgaacggat tgaagaaacg caaaaagtgt      420
ctacggactt taaattaaa atg gaa aaa tat gaa aac ctg ggt ttg gtt gga      472
                Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly
                1                5                10
gaa ggg agt tat gga atg gtg atg aag tgt agg aat aaa gat act gga      520
Glu Gly Ser Tyr Gly Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly
                15                20                25
aga att gtg gcc ata aag aag ttc tta gaa agt gac gat gac aaa atg      568
Arg Ile Val Ala Ile Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met
                30                35                40
gtt aaa aag att gca atg cga gaa gtc aag tta cta aag caa ctt agg      616

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Val	Lys	Lys	Ile	Ala	Met	Arg	Glu	Val	Lys	Leu	Leu	Lys	Gln	Leu	Arg	
45					50					55						
cat	gaa	aac	ttg	gtg	aat	ctc	ttg	gaa	gtg	tgt	aaa	aaa	aaa	a		659
His	Glu	Asn	Leu	Val	Asn	Leu	Leu	Glu	Val	Cys	Lys	Lys	Lys			
60					65					70						

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 <213> Homo sapiens

<220>
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 <222> 38..283

<221> sig_peptide
 <222> 38..85
 <223> Von Heijne matrix
 score 4.1
 seq LLPATSLAGPVLS/TL

<221> polyA_signal
 <222> 257..262

<400> 127																	
cac	ctg	aatc	ccagga	accc	tcaatg	agggt	cttcaag	atg	aag	aga	ctg	ctg	cca			55	
								Met	Lys	Arg	Leu	Leu	Pro				
								-15									
gct	acc	agc	ctg	gct	ggc	cct	gtc	ctg	tcc	acc	ctc	att	gcc	cca	act	103	
Ala	Thr	Ser	Leu	Ala	Gly	Pro	Val	Leu	Ser	Thr	Leu	Ile	Ala	Pro	Thr		
-10					-5			1					5				
ccc	atg	ttg	ttt	tgt	gaa	gat	aaa	agc	tgg	gat	ctt	ttt	ctt	ttt	ttt	151	
Pro	Met	Leu	Phe	Cys	Glu	Asp	Lys	Ser	Trp	Asp	Leu	Phe	Leu	Phe	Phe		
			10					15					20				
aag	tct	cac	aag	aca	tgg	ggc	atc	tcc	aca	aat	tta	agt	tcc	tgt	cca	199	
Lys	Ser	His	Lys	Thr	Trp	Gly	Ile	Ser	Thr	Asn	Leu	Ser	Ser	Cys	Pro		
			25				30				35						
ttt	gga	aat	ttg	ttt	cta	tgt	gta	cag	ttt	gtc	aga	gaa	aaa	caa	agt	247	
Phe	Gly	Asn	Leu	Phe	Leu	Cys	Val	Gln	Phe	Val	Arg	Glu	Lys	Gln	Ser		
			40				45				50						
ttt	tgt	atg	aat	aca	gaa	tgt	gat	tta	cgc	aag	aat	tgac	aaaaaaa			293	
Phe	Cys	Met	Asn	Thr	Glu	Cys	Asp	Leu	Arg	Lys	Asn						
55					60						65						
aaaaaaa																301	

<210> 128
 <211> 477
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..477

<221> sig_peptide
 <222> 121..288
 <223> Von Heijne matrix
 score 3.5
 seq SSCADSFVSSSSS/QP

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 cctccctctc tcccccccg tatctctttt cacccttctc ccaccctcgc tcgcgtagcc 120
 atg gcg gag ccg tcg gcg gcc act cag tcc cat tcc atc tcc tcg tcg 168
 Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
 -55 -50 -45
 tcc ttc gga gcc gag ccg tcc gcg ccc ggc ggc ggc ggc agc cca gga 216
 Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Gly Ser Pro Gly
 -40 -35 -30 -25
 gcc tgc ccc gcc ctg ggg acg aag agc tgc agc tcc tcc tgt gcg gat 264
 Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
 -20 -15 -10
 tcc ttt gtt tct tcc tct tcc tct cag cct gta tct cta ttt tcg acc 312
 Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
 -5 1 5
 tca caa gag gga ttg agc tct ctt tgc tct gat gag cca tct tca gaa 360
 Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
 10 15 20
 att atg act tct tcc ttt ctt tca tct tct gaa ata cat aac act ggc 408
 Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
 25 30 35 40
 ctt aca ata cta cat gga gaa aaa agc cat gtg tta ggg agc cag cct 456
 Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
 45 50 55
 att tta gcc aaa aaa aaa aaa 477
 Ile Leu Ala Lys Lys Lys Lys
 60

<210> 129
 <211> 323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..163

<221> polyA_signal
 <222> 292..297

<221> polyA_site
 <222> 310..323

<400> 129
 a gct ttc gtg tgg gag cca gct atg gtg cgg atc aat gcg ctg aca gca 49
 Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
 1 5 10 15
 gcc tct gag gct gcg tgc ctg atc gtg tct gta gat gaa acc atc aag 97

Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys	
20 25 30	
aac ccc cgc tcg act gtg gat gct ccc aca gca gca ggc cgg ggc cgt	145
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg	
35 40 45	
ggc cgt ggc cgc ccc cac tgagaggcac cccacccatc acatggctgg	193
Gly Arg Gly Arg Pro His	
50	
ctggctgctg ggtgcactta ccctccttgg cttgggttact tcattttaca aggaaggggt	253
agtaattggc ccactctctt ctactggag gctatttaaa taaaatgtaa gacttcaaaa	313
aaaaaaaaa	323

<210> 130
 <211> 1392
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 46..675

<221> sig_peptide
 <222> 46..87
 <223> Von Heijne matrix
 score 5.3
 seq LTLGLSFILAGL/IV

<221> polyA_signal
 <222> 1364..1369

<221> polyA_site
 <222> 1383..1392

<400> 130	
ctccgagttg ccaccagga aaaagagggc tcctctggga gatgt atg ctt act ctc	57
Met Leu Thr Leu	
tta ggc ctt tca ttc atc ttg gca gga ctt att gtt ggt gga gcc tgc	105
Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys	
-10 -5 1 5	
att tac aag tac ttc atg ccc aag agc acc att tac cgt gga gag atg	153
Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met	
10 15 20	
tgc ttt ttt gat tct gag gat cct gca aat tcc ctt cgt gga gga gag	201
Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu	
25 30 35	
cct aac ttc ctg cct gtg act gag gag gct gac att cgt gag gat gac	249
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp Asp	
40 45 50	
aac att gca atc att gat gtg cct gtc ccc agt ttc tct gat agt gac	297
Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp Ser Asp	
55 60 65 70	
cct gca gca att att cat gac ttt gaa aag gga atg act gct tac ctg	345
Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr Ala Tyr Leu	
75 80 85	
gac ttg ttg ctg ggg atc tgc tat ctg atg ccc ctc aat act tct att	393

Asp	Leu	Leu	Leu	Gly	Ile	Cys	Tyr	Leu	Met	Pro	Leu	Asn	Thr	Ser	Ile	
			90					95					100			
gtt	atg	cct	cca	aaa	aat	ctg	gta	gag	ctc	ttt	ggc	aaa	ctg	gcg	agt	441
Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe	Gly	Lys	Leu	Ala	Ser	
		105					110				115					
ggc	aga	tat	ctg	cct	caa	act	tat	gtg	gtt	cga	gaa	gac	cta	gtt	gct	489
Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val	Arg	Glu	Asp	Leu	Val	Ala	
	120				125			130								
gtg	gag	gaa	att	cgt	gat	gtt	agt	aac	ctt	ggc	atc	ttt	att	tac	caa	537
Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn	Leu	Gly	Ile	Phe	Ile	Tyr	Gln	
	135			140				145						150		
ctt	tgc	aat	aac	aga	aag	tcc	ttc	cgc	ctt	cgt	cgc	aga	gac	ctc	ttg	585
Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe	Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	
			155					160					165			
ctg	ggt	ttc	aac	aaa	cgt	gcc	att	gat	aaa	tgc	tgg	aag	att	aga	cac	633
Leu	Gly	Phe	Asn	Lys	Arg	Ala	Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	
		170						175				180				
ttc	ccc	aac	gaa	ttt	att	gtt	gag	acc	aag	atc	tgt	caa	gag			675
Phe	Pro	Asn	Glu	Phe	Ile	Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu			
		185				190					195					
taagaggcaa	cagatagagt	gtccttggtg	ataagaagtc	agagatttac	aatatgactt											735
taacattaag	gtttatggga	tactcaagat	atttactcat	gcatttactc	tattgcttat											795
gctttaaaaa	aaggaaaaaa	aaaaaactac	taaccactgc	aagctcttgt	caaatttttag											855
tttaattggc	attgcttggt	ttttgaaact	gaaattacat	gagtttcatt	ttttctttgc											915
atttataggg	tttagatttc	tgaaagcagc	atgaatata	cacctaacat	cctgacaata											975
aattccatcc	gttggttttt	ttgtttgttt	gttttttctt	ttcctttaag	taagctcttt											1035
attcatctta	tggtgggagca	attttaaaa	ttgaaatatt	ttaaattggt	tttgaacttt											1095
ttgtgtaaaa	tatatcagat	ctcaacattg	ttggtttctt	ttgtttttca	ttttgtacaa											1155
ctttcttgaa	tttagaaatt	acatctttgc	agttctgtta	ggtgctctgt	aattaacctg											1215
acttatatgt	gaacaatttt	catgagacag	tcatttttaa	ctaatagcagt	gattctttct											1275
cactactatc	tgtattgtgg	aatgcacaaa	attgtgtagg	tgctgaatgc	tgtaaggagt											1335
ttaggttgta	tgaattctac	aaccctataa	taaattttac	tctatacaaa	aaaaaaa											1392

<210> 131

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 62..385

<221> polyA_signal

<222> 974..979

<221> polyA_site

<222> 987..999

<400> 131

cctgaatgac	ttgaatgttt	ccccgcctga	gctaacagtc	catgtgggtg	attcagctct		60										
g	atg	gga	tgt	gtt	ttc	cag	agc	aca	gaa	gac	aaa	tgt	ata	ttc	aag	ata	109
Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile		
1			5					10					15				
gac	tgg	act	ctg	tca	cca	gga	gag	cac	gcc	aag	gac	gaa	tat	gtg	cta		157
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu		

	20		25		30	
tac tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc						205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg						
	35		40		45	
gta cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc						253
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu						
	50		55		60	
caa gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc						301
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg						
	65		70		75	80
ctc aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg						349
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val						
	85		90		95	
ctt cca gag gag ccc aaa ggt acg caa atg ctt act taaagagggg						395
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr						
	100		105			
ccaaggggca agagctttca tgtgcaagag gcaaggaaac tgattatctt gagtaaattgc						455
cagccttttg gctaagtact taccacagag tgaatcttca aaaaatgatc ataattattt						515
cagtcaataa aaatagagtt attttattaa ataaaaatatt gataattatt gtattattac						575
tttaaacaca cttccccctc acaaaagccc tgtgaaggat gttttgttca catatatgtc						635
caaatatgtt ttggacacat atttatttaa tggaataaat agtacttgaa ccctggcacc						695
tctgacaaca aagtccatgt tcttttttact atgccctaac acctttcatc agttatccac						755
tattgatgcta catctgtatt ttataggtac cctatgttag gtgttctggg ggatagaaaa						815
gaaataagca ggccaggctc agtggctcat gcctgtaatc ctagcatttt gggaggctga						875
ggcagcagaa ctgcctgagc cccagggttc aagactgcag tgagctatga tggcaccact						935
gcattctagc ctgggtgaca gagcaagact ctgtctaaaa taaaaaaga gaaaaaaaaa						995
aaaa						999

<210> 132

<211> 725

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 422..550

<221> sig_peptide

<222> 422..475

<223> Von Heijne matrix

score 4.5

seq LRWLMPVIPALWG/AE

<221> polyA_site

<222> 714..725

<400> 132

tctgcgaggg tgggagagaa aattaggggg agaaaggaca gagagagcaa ctaccatcca	60
tagccagata ggtgagtaaa tatatttgca gtaacctatt tgctattcct tgctgcaact	120
gtgtttaatg ttccttccag aatcagagag agtattgcca tccaagaaat cgtttttaga	180
tatgacattt gagctatcat cttgagacca atacctaaaa caatttcagt ttaagaaatg	240
tctaggatat gtgaaaacac agtttaaaac cagcaaaaca gaatttattg ccctcagcga	300
ataccacaa tgtacatata ccttgtattt ctgaaagcaa agcaagcatg ccaagtagtt	360
tttatttacc tgtacctata atacagcaag gtgaaacagg atatattttt gaagtttaaa	420
a atg tct tca ggc cgg ctg cgg tgg ctc atg cct gta atc cca gca ctt	469

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Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
      -15          -10          -5
tgg gga gcc gag aag ggt gaa tca cct gag gtc agc agt ttt gag acc      517
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
      1          5          10
agg ctg gcc aac atg gcg aaa ccc tgt ctc tac tgaaaataca aaaattagct      570
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
      15          20          25
gggtgtggtg gcgggcgcct gtagtcccag ctacttggga gactgaggca ggagaattgc      630
ttgaacacgg aaggcggaag ttgcagtaag ctgagatcgt gccaccgcac accagcttgg      690
gcaacagagt gagactccct ctcaaaaaaa aaaaaa      725

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<210> 133
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..231

<221> polyA_site
 <222> 387..400

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<400> 133
ctcgcctctc ctggcttctg gtatgcacca gcaattcctg gcgttccttg gctcctagaa      60
gcatactacc tatcacatgg tcattcttcac cctgtgtgtc ttcacactac cttttctctg      120
atg atg tct gcc cga atc cct ttt tat aag gac acc agt cag att aga      168
Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg
      1          5          10          15
tta ggg tct acc ata ata cct cat ttt aac tta atc acc ttt gta aag      216
Leu Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys
      20          25          30
acc ttt ttc caa ata tagtcactct ctgagggtact gatgggttagg atctcaacat      271
Thr Phe Phe Gln Ile
      35
accttttttg ggaggacaca attgaaccca taacagggtg tttgcaagga agagttaaaa      331
tttgaaagaa aggtgggtatt tgcttagata gatagggcac agctttctag gtgacaaaaa      391
aaaaaaaaa      400

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<210> 134
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 131..1051

<221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix
 score 4.2

<222> 1019..1024

<400> 134

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tgatggccag	gccccggagg	ctaaggacgg	cagctccttt	agcggcagag	ttttccgagt		120									
gacctttcttg	atg	ctg	gct	gtt	tct	ctc	acc	gtt	ccc	ctg	ctt	gga	gcc		169	
	Met	Leu	Ala	Val	Ser	Leu	Thr	Val	Pro	Leu	Leu	Gly	Ala			
				-10					-5							
atg	atg	ctg	ctg	gaa	tct	cct	ata	gat	cca	cag	cct	ctc	agc	ttc	aaa	217
Met	Met	Leu	Leu	Glu	Ser	Pro	Ile	Asp	Pro	Gln	Pro	Leu	Ser	Phe	Lys	
1				5					10					15		
gaa	ccc	ccg	ctc	ttg	ctt	ggg	gtt	ctg	cat	cca	aat	acg	aag	ctg	cga	265
Glu	Pro	Pro	Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	
			20					25					30			
cag	gca	gaa	agg	ctg	ttt	gaa	aat	caa	ctt	gtt	gga	ccg	gag	tcc	ata	313
Gln	Ala	Glu	Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	
		35					40					45				
gca	cat	att	ggg	gat	gtg	atg	ttt	act	ggg	aca	gca	gat	ggc	cgg	gtc	361
Ala	His	Ile	Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	
	50					55					60					
gta	aaa	ctt	gaa	aat	ggg	gaa	ata	gag	acc	att	gcc	cgg	ttt	ggg	tcg	409
Val	Lys	Leu	Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	
65					70					75				80		
ggc	cct	tgc	aaa	acc	cga	gat	gat	gag	cct	gtg	tgt	ggg	aga	ccc	ctg	457
Gly	Pro	Cys	Lys	Thr	Arg	Asp	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	
				85					90					95		
ggg	atc	cgt	gca	ggg	ccc	aat	ggg	act	ctc	ttt	gtg	gcc	gat	gca	tgc	505
Gly	Ile	Arg	Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Cys	
			100					105					110			
aag	gga	cta	ttt	gaa	gta	aat	ccc	tgg	aaa	cgt	gaa	gtg	aaa	ctg	ctg	553
Lys	Gly	Leu	Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	
		115					120					125				
ctg	tcc	tcc	gag	aca	ccc	att	gag	ggg	aag	aac	atg	tcc	ttt	gtg	aat	601
Leu	Ser	Ser	Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	
		130				135					140					
gat	ctt	aca	gtc	tct	cag	gat	ggg	agg	aag	att	tat	ttc	acc	gat	tct	649
Asp	Leu	Thr	Val	Ser	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	
145				150						155				160		
agc	agc	aaa	tgg	caa	aga	cga	gac	tac	ctg	ctt	ctg	gtg	atg	gag	ggc	697
Ser	Ser	Lys	Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly	
				165					170					175		
aca	gat	gac	ggg	cgc	ctg	ctg	gag	tat	gat	act	gtg	acc	agg	gaa	gta	745
Thr	Asp	Asp	Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	
			180					185	</							

Val	Glu	Asn	Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser		
				245					250					255			
ggg	ggg	tac	tgg	gtg	ggc	atg	tcg	acc	atc	cgc	cct	aac	cct	ggg	ttt		985
Gly	Gly	Tyr	Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe		
			260					265					270				
tcc	atg	ctg	gat	ttc	tta	tct	gag	aga	ccc	tgg	att	aaa	agg	atg	att		1033
Ser	Met	Leu	Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile		
		275					280					285					
ttt	aag	gca	aaa	aaa	aaa	aa											1053
Phe	Lys	Ala	Lys	Lys	Lys												
		290															

<210> 135
 <211> 1128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..403

<221> sig_peptide
 <222> 86..181
 <223> Von Heijne matrix
 score 8.8
 seq VPMLLLIVGGSFG/LR

<221> polyA_signal
 <222> 1097..1102

<221> polyA_site
 <222> 1117..1128

<400> 135																	
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ctctgagccga	tggaagagtt	cactc	atg	ttt	gca	ccc	gcg	gtg	atg	cgt	gct						112
		Met	Phe	Ala	Pro	Ala	Val	Met	Arg	Ala							
				-30					-25								
ttt	cgc	aag	aac	aag	act	ctc	ggc	tat	gga	gtc	ccc	atg	ttg	ttg	ctg		160
Phe	Arg	Lys	Asn	Lys	Thr	Leu	Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu		
		-20					-15						-10				
att	gtt	gga	ggt	tct	ttt	ggt	ctt	cgt	gag	ttt	tct	caa	atc	cga	tat		208
Ile	Val	Gly	Gly	Ser	Phe	Gly	Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr		
		-5				1			5								
gat	gct	gtg	aag	agt	aaa	atg	gat	cct	gag	ctt	gaa	aaa	aaa	ctg	aaa		256
Asp	Ala	Val	Lys	Ser	Lys	Met	Asp	Pro	Glu	Leu	Glu	Lys	Lys	Leu	Lys		
10				15				20						25			
gag	aat	aaa	ata	tct	tta	gag	tcg	gaa	tat	gag	aaa	atc	aaa	gac	tcc		304
Glu	Asn	Lys	Ile	Ser	Leu	Glu	Ser	Glu	Tyr	Glu	Lys	Ile	Lys	Asp	Ser		
			30					35						40			
aag	ttt	gat	gac	tgg	aag	aat	att	cga	gga	ccc	agg	cct	tgg	gaa	gat		352
Lys	Phe	Asp	Asp	Trp	Lys	Asn	Ile	Arg	Gly	Pro	Arg	Pro	Trp	Glu	Asp		
		45						50					55				
cct	gac	ctc	ctc	caa	gga	aga	aat	cca	gaa	agc	ctt	aag	act	aag	aca		400
Pro	Asp	Leu	Leu	Gln	Gly	Arg	Asn	Pro	Glu	Ser	Leu	Lys	Thr	Lys	Thr		

60	65	70	
act tgactctgct gattcttttt tccnnntttt ttttttttta aataaaaata			453
Thr			
ctattaactg gacttcctaa tatatacttc tatcaagtgg aaaggaaatt ccaggcccat			513
ggaaacttgg atatgggtaa tttgatgaca aataatcttc actaaaggtc atgtacaggt			573
ttttatactt cccagctatt ccatctgtgg atgaaagtaa caatgttggc cacgtatatt			633
ttacacctcg aaataaaaaa tgtgaatact gctccaaaaa aaaaaaccag taccgtgtag			693
tctctctcgt ggcttggatt tacctgggc aacgtggttg gaatgtatct ggctcagaac			753
tatgatatac caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag			813
aagaaacccc ctagtgcatt agactgcctc cagcactgcc ttcaggatat accgattcta			873
ctgctcttga gggcctcgtt tactatctga accaaaagct tttgttttcg tctccagcct			933
cagcacttct cttctttgct agaccctgtg ttttttgctt taaagcaagc aaaatggggc			993
cccaatttga gaactaccct acgtttccaa catactcacc tcttcccata atccctttcc			1053
aactgcatgg gaggttctaa gactggaatt atggtgctag attagtaaac atgactttta			1113
acgaaaaaaa aaaaa			1128

<210> 136

<211> 254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 37..162

<221> sig_peptide

<222> 37..93

<223> Von Heijne matrix

score 9.5

seq LMCLSLCTAFALS/KP

<221> polyA_signal

<222> 224..229

<221> polyA_site

<222> 243..254

<400> 136

tgtgctgtgg gggctacgag gaaagatcta attatc atg gac ctg cga cag ttt	54
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Met Asp Leu Arg Gln Phe

-15

ctt atg tgc ctg tcc ctg tgc aca gcc ttt gcc ttg agc aaa ccc aca	102
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Leu Met Cys Leu Ser Leu Cys Thr Ala Phe Ala Leu Ser Lys Pro Thr

-10

-5

1

gaa aag aag gac cgt gta cat cat gag cct cag ctc agt gac aag gtt	150
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Glu Lys Lys Asp Arg Val His His Glu Pro Gln Leu Ser Asp Lys Val

5

10

15

cac aat gat att tgatagaacc aattgttgta cataaaacag atctgcgcatt	202
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His Asn Asp Ile

20

atatatatat gtataaaaaa taataaaaata atggaagatg aaaaaaaaaa aa	254
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<210> 137

<211> 886
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..381

<221> sig_peptide
<222> 31..90
<223> Von Heijne matrix
score 5.4
seq AFVIACVLSLIST/IY

<221> polyA_site
<222> 875..886

<400> 137

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ggaggatggg cgagcagtct gaatggcaga atg gat aac cgt ttt gct aca gca      54
                               Met Asp Asn Arg Phe Ala Thr Ala
                               -20                               -15
ttt gta att gct tgt gtg ctt agc ctc att tcc acc atc tac atg gca      102
Phe Val Ile Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala
                               -10                               -5                               1
gcc tcc att ggc aca gac ttc tgg tat gaa tat cga agt cca gtt caa      150
Ala Ser Ile Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln
5                               10                               15                               20
gaa aat tcc agt gat ttg aat aaa agc atc tgg gat gaa ttc att agt      198
Glu Asn Ser Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser
                               25                               30                               35
gat gag gca gat gaa aag act tat aat gat gca ctt ttt cga tac aat      246
Asp Glu Ala Asp Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn
                               40                               45                               50
ggc aca gtg gga ttg tgg gga cgg tgt atc acc ata ccc aaa aac atg      294
Gly Thr Val Gly Leu Trp Gly Arg Cys Ile Thr Ile Pro Lys Asn Met
55                               60                               65
cat tgg tat agc cca cca gaa agg aca ggt att tct ctt att tta act      342
His Trp Tyr Ser Pro Pro Glu Arg Thr Gly Ile Ser Leu Ile Leu Thr
70                               75                               80
tct gtc ttc ttc acc tgg tta ata ata gac aaa acg acg taatgattgc      391
Ser Val Phe Phe Thr Trp Leu Ile Ile Asp Lys Thr Thr
85                               90                               95
ccaattacat gtaagcagggt ttgttggttc tctctctcct taaagaaata aatcgtgtat      451
cttctctttc tactgccttc tctccccaac ttctttgcat taccatggta ctcacatcaata      511
ttggttggtat gaggaacttt tcttatcttg ggaaagcctt aatggccttt ttttttctta      571
tttactcact cattaaaata cttttcatta ctctaacaca tggtataaag aaatagttagg      631
aaaagtgcac cgaaagactt ttaaaaatat ttggttaacta gtaaaaggac taccatcgaa      691
aatcaactca aaaaattgtc cttttatggg ttagctgtat tataatacat atctatcatt      751
tgccctgtg tcttagagga tataatttga ccagctctac atttaatctg tgtaattatg      811
agactgtttt acaacaatct tgatgcagag ttggtagggtt aagaaatttg tattacagaa      871
gttaaaaaaa aaaaaa                                         886

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<210> 138
<211> 1244
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..579

<221> sig_peptide

<222> 46..156

<223> Von Heijne matrix

score 3.5

seq LVFNFLILTILT/IW

<400> 138

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cccttatcca ggttnttatc tanggaatcc cnnnaagact gggga atg gag aga cag      57
                                         Met Glu Arg Gln
                                         -35
tca agg gtt atg tca gaa aag gat gag tat cag ttt caa cat can nna      105
Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe Gln His Xaa Xaa
          -30                      -25                      -20
gcg gng gan ctg ctt gtc ttc aat ttt ttg ctc atc ctt acc att ttg      153
Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile Leu Thr Ile Leu
          -15                      -10                      -5
aca atc tgg tta ttt aaa aat cat cga ttc cgc ttc ttg cat gaa act      201
Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe Leu His Glu Thr
          1                      5                      10                      15
gga gga gca atg gtg tat ggc ctt ata atg gga cta att tca cga tat      249
Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu Ile Ser Arg Tyr
          20                      25                      30
gct aca gca cca act gat att gaa agt gga act gtc tgt gac tgt gta      297
Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val Cys Asp Cys Val
          35                      40                      45
aaa cta act ttc agt cca cca act ctg ctg gtt aat gtc act gac caa      345
Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn Val Thr Asp Gln
          50                      55                      60
gtt tat gaa tat aaa tac aaa aga gaa ata agt cag cac aac atc aat      393
Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln His Asn Ile Asn
          65                      70                      75
cct cat caa gga aat gct ata ctt gaa aag atg aca ttt gat cca gaa      441
Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr Phe Asp Pro Glu
          80                      85                      90                      95
atc ttc ttc aat gtt tta ctg cca cca att ata ttt cat gca gga tat      489
Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe His Ala Gly Tyr
          100                      105                      110
agt cta aag aag aga cac ttt ttt caa aac tta gga tct att tta acg      537
Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly Ser Ile Leu Thr
          115                      120                      125
tat gcc ttc ttg gga act gcc atc tcc tgc atc gtc ata ggg      579
Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val Ile Gly
          130                      135                      140
taagtacat tccgagctca agttgcaggt ggctgtgggg tctgtgatct gtgtgagggga      639
tctaacactt ccaggattct tgctggctgg gaaaattgtc ttttttttag tatatcacat      699
atttgatatg tttttctgac ttaattccac ggcttctgac aaatacaagg cttcaaatca      759
aagcaaacta gaggattgct ggactttctc tgtgagttct ggacttctga cttaggggaat      819
gtggatcact tgccttgagt tatgtgaagc gcattgcatt cttcttttag tttgagtaat      879
gccgatatgg tcactgcatt cttttttgtc ttgtattgag agaccttacc tgtatttggc      939
aggagtgc aaagtaactat atgccaaagag ttttctttct aaaggaaagt ttacaagaca      999
gcagtctgaa acagatatgn tccaaatatn naacagagtt gcttaataca gggatagctt      1059
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ttcagttaat accctgtaga atgcagactc tttnttttcat tgtatttttct tgattatgct	1119
actgagccct aagtcacacg ttatatactc tggcttgcag ctcatcataa agtaaaatgt	1179
ggtaccaa at ggtgaaggca atccagcctn tgataatccc gtccaataca ttaaagntcc	1239
actgc	1244

<210> 139
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..469

<221> sig_peptide
 <222> 92..172
 <223> Von Heijne matrix
 score 7.9
 seq VVVLALGFLGCGY/AK

<221> polyA_signal
 <222> 454..459

<221> polyA_site
 <222> 458..471

<400> 139	
gcaagtgcag aagtcggtga cggtgggcat ctgggtgtca atcgatgggg catcctttct	60
gaagatcttc gggccactgt cgtccagtgc c atg cag ttt gtc aac gtg ggc	112
	Met Gln Phe Val Asn Val Gly
	-25
tac ttc ctc atc gca gcc ggc gtt gtg gtc ctt gct ctt ggt ttc ctg	160
Tyr Phe Leu Ile Ala Ala Gly Val Val Val Leu Ala Leu Gly Phe Leu	
	-15 -10 -5
ggc tgc tat ggt gct aag act gag agc atg tgt gcc ctc gtg acg ttc	208
Gly Cys Tyr Gly Ala Lys Thr Glu Ser Met Cys Ala Leu Val Thr Phe	
	1 5 10
ttc ttc atc ctc ctc ctc atc ttc att gct gag gtt gca gct gct gtg	256
Phe Phe Ile Leu Leu Leu Ile Phe Ile Ala Glu Val Ala Ala Ala Val	
	15 20 25
gtc gcc ctg gtg tac acc aca atg gct gag cac ttc ctg acg ttg ctg	304
Val Ala Leu Val Tyr Thr Thr Met Ala Glu His Phe Leu Thr Leu Leu	
	30 35 40
gta gtg cct gcc atc aag aaa gat tat ggt tcc cag gaa gac ttc act	352
Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp Phe Thr	
	45 50 55 60
caa gtg tgg aac acc acc atg aaa ggg ctc aag tgc cgt ggc ttc acc	400
Gln Val Trp Asn Thr Thr Met Lys Gly Leu Lys Cys Arg Gly Phe Thr	
	65 70 75
aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg cat aaa cct	448
Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met His Lys Pro	
	80 85 90
gtt aca atg atg aaa aaa aaa aa	471
Val Thr Met Lys Lys Lys Lys	
	95

<210> 140
<211> 849
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..675

<221> sig_peptide
<222> 154..498
<223> Von Heijne matrix
score 4.8
seq PLRLNLLILIEG/GV

<221> polyA_signal
<222> 819..824

<221> polyA_site
<222> 838..849

<400> 140
ccccctatctc cagacctcat tcgcaatgaa gtagaatgtc tgaaagcaga tttcaaccac 60
agaatcaagg aggttctctt caactccctc ttcagtgcct actatgttgc atttctcccc 120
ctgtgttttg tgaagagtac ccagtactat gac atg cgc tgg tca tgt gag cac 174
Met Arg Trp Ser Cys Glu His
-115 -110
ctc gtt atg gtg tgg atc aat gct ttt gtc atg ctc acc acg caa ctg 222
Leu Val Met Val Trp Ile Asn Ala Phe Val Met Leu Thr Thr Gln Leu
-105 -100 -95
ttg cca tcc aaa tac tgt gat ttg cta cat aaa tca gct gct cac ctg 270
Leu Pro Ser Lys Tyr Cys Asp Leu Leu His Lys Ser Ala Ala His Leu
-90 -85 -80
ggc aag tgg cag aag ttg gaa cat ggg tcc tac agc aat gct cca cag 318
Gly Lys Trp Gln Lys Leu Glu His Gly Ser Tyr Ser Asn Ala Pro Gln
-75 -70 -65
cac att tgg tca gaa aat aca ata tgg cct caa ggg gtg ctg gtg cgg 366
His Ile Trp Ser Glu Asn Thr Ile Trp Pro Gln Gly Val Leu Val Arg
-60 -55 -50 -45
cac agc aga tgt tta tat aga gcc atg ggg cct tac aac gtg gca gtg 414
His Ser Arg Cys Leu Tyr Arg Ala Met Gly Pro Tyr Asn Val Ala Val
-40 -35 -30
cct tca gat gta tct cat gcc cgc ttt tat ttc tta ttt cat cga cca 462
Pro Ser Asp Val Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro
-25 -20 -15
tta agg ctg tta aat ctg ctc atc ctt att gag ggc ggt gtc gtc ttc 510
Leu Arg Leu Leu Asn Leu Leu Ile Leu Ile Glu Gly Gly Val Val Phe
-10 -5 1
tat cag ctc tat tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt 558
Tyr Gln Leu Tyr Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu
5 10 15 20
tcc atg gct ctc atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt 606
Ser Met Ala Leu Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu
25 30 35

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ctc cgg gac aga ata gta tta ggc agg gca tac tcc tac cca ctc aac      654
Leu Arg Asp Arg Ile Val Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn
      40      45      50
agt tat gaa ctc aag gca aac taagctgcct ctcaacaatg agggagaact      705
Ser Tyr Glu Leu Lys Ala Asn
      55
cagataaaaaa tattttcata cgttctatatt ttttcttgtg atttttataa atatttaaga      765
tgttttatat tttgtataact attatgtttt gaaagtcggg aagagtaagg gatattaaat      825
gtatccgtaa acaaaaaaaaaa aaaa      849

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<210> 141
 <211> 155
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

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<400> 141
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
  -30      -25      -20
Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
  -15      -10      -5      1
Leu Leu Pro His Cys Gln Lys Pro Phe Val Tyr Asp Leu His Ala Val
      5      10      15
Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
      20      25      30
Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
  35      40      45
Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
  50      55      60      65
Leu Gly Thr Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
      70      75      80
Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
      85      90      95
Gly Leu Ile Phe Cys Cys Ala Phe Cys Ser Glu Thr Lys Leu Phe Leu
      100      105      110
Ser Arg Gln Ala Met Ala Glu Asn Phe Ser Ile
      115      120

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<210> 142
 <211> 55
 <212> PRT
 <213> Homo sapiens

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<400> 142
Met Ala Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys Arg
  1      5      10      15
Met Tyr Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe
      20      25      30
Phe Met Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln
      35      40      45

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Lys Gln Lys Lys Arg Ser Asn
50 55

<210> 143
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 143
Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
-20 -15 -10 -5
Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
1 5 10
Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
15 20 25
Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
30 35 40
Gly Arg Lys
5

<210> 144
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 144
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val Thr
-20 -15 -10
Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala Gln His
-5 1 5 10
Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly Gln Ala
15 20 25
Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Trp Leu Thr Lys Ala Arg
30 35 40
Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly Gln Glu
45 50 55
Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser Leu Leu
60 65 70 75
Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu Ala Thr
80 85 90
Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu Arg Asp
95 100 105
Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu Gly Pro
110 115 120
Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys Gln Ser

125		130		135
His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu				
140		145		150
Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His				
		160		165
Thr Ala Ala Leu Pro Ala				170
		175		

<210> 145
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 145	
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met	
-25	-20
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser	-15
	-5
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp	1
	10
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Lys Xaa	15
	20
Ala Gly Leu Gln Ser Ser Gly Lys Glu Ala Ala Leu Asn Leu Ser Phe	25
	30
Ile Ser Lys Glu Glu Met Lys Asn Thr Ser Trp Ile Arg Lys Asn Trp	35
	40
Leu Leu Val Ala Gly Ile Ser Phe Ile Gly Asp His Leu Gly Thr Tyr	45
	50
Phe Leu Gln Arg Ser Ala Lys Gln Ser Val Lys Phe Gln Ser Gln Ser	55
	60
Lys Gln Lys Ser Ile Glu Glu	65
	70
	75
	80
	85
	90
	95
	100
	105
	110

<210> 146
 <211> 255
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -70...-1

<400> 146	
Met Gln Gln Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe	
-70	-65
Pro Gln Ile Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val	-60
	-50
Ile Ala Asn Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn	-45
	-40
	-35
	-30
	-25

Val	Val	Ser	Gly	Ser	Thr	Gly	Ile	Leu	Ser	Val	Ile	Gly	Val	Met	Leu
		-20					-15					-10			
Ala	Pro	Phe	Thr	Ala	Gly	Leu	Ser	Leu	Ser	Ile	Thr	Ala	Ala	Gly	Val
	-5					1				5					10
Gly	Leu	Gly	Ile	Ala	Ser	Ala	Thr	Ala	Gly	Ile	Ala	Ser	Ser	Ile	Val
				15					20					25	
Glu	Asn	Thr	Tyr	Thr	Arg	Ser	Ala	Glu	Leu	Thr	Ala	Ser	Arg	Leu	Thr
			30					35					40		
Ala	Thr	Ser	Thr	Asp	Gln	Leu	Glu	Ala	Leu	Arg	Asp	Ile	Leu	His	Asp
		45					50					55			
Ile	Thr	Pro	Asn	Val	Leu	Ser	Phe	Ala	Leu	Asp	Phe	Asp	Glu	Ala	Thr
	60					65				70					
Lys	Met	Ile	Ala	Asn	Asp	Val	His	Thr	Leu	Arg	Arg	Ser	Lys	Ala	Thr
	75				80					85					90
Val	Gly	Arg	Pro	Leu	Ile	Ala	Trp	Arg	Tyr	Val	Pro	Ile	Asn	Val	Val
				95					100					105	
Glu	Thr	Leu	Arg	Thr	Arg	Gly	Ala	Pro	Thr	Arg	Ile	Val	Arg	Lys	Val
			110					115					120		
Ala	Arg	Asn	Leu	Gly	Lys	Ala	Thr	Ser	Gly	Val	Leu	Val	Val	Leu	Asp
		125					130					135			
Val	Val	Asn	Leu	Val	Gln	Asp	Ser	Leu	Asp	Leu	His	Lys	Gly	Glu	Lys
	140					145					150				
Ser	Glu	Ser	Ala	Glu	Leu	Leu	Arg	Gln	Trp	Ala	Gln	Glu	Leu	Glu	Glu
	155				160				165						170
Asn	Leu	Asn	Glu	Leu	Thr	His	Ile	His	Gln	Ser	Leu	Lys	Ala	Gly	
				175					180					185	

<210> 147
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

Met	Pro	Gly	Thr	Glu	Val	Leu	Glu	Gly	Ala	Thr	Asp	Gly	Leu	Ala	Ala
				-45					-40					-35	
Ile	Asn	Leu	Leu	Lys	Trp	Ile	Lys	Thr	Leu	Gly	Gly	Ser	Val	Ile	Ser
			-30					-25					-20		
Met	Ile	Val	Leu	Leu	Ile	Cys	Val	Val	Cys	Leu	Tyr	Ile	Val	Cys	Arg
		-15				-10						-5			
Cys	Gly	Ser	His	Leu	Trp	Arg	Glu	Ser	His	His					
	1				5					10					

<210> 148
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln Leu

1				5						10					15				
Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly	Asp	Gly				
			20					25					30						
Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln	Leu	Ser	Ala				
		35					40					45							
Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Ile	Pro	Tyr	Gly	Ser	Arg	His				
	50					55					60								
Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu	Tyr	Leu	Glu	Thr	Lys				
65					70					75					80				
Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser	Leu	Ser	Ser	Thr	Gly	Thr				
				85					90					95					
Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp	Phe	Gln	Lys	Phe	Pro	Asp	Lys				
			100					105					110						
Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro	Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys				
		115					120					125							
Ile	Arg	Asn	Ser	Gly	Ser	Ala	Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr				
	130					135					140								
Gln	Pro	Ile	Ile	His	Arg	Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser				
145					150					155					160				
Ala	Thr	Cys	Gly	Gly	Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp				
			165						170					175					

Leu Arg Ser Asn
180

<210> 149
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 149

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala	Ala				
			-20					-15					-10						
Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro	Ser	Leu				
			-5				1				5								
Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys	Glu	Cys	Phe				
10					15					20					25				
Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile	Glu	Tyr	Gln	Val				
				30					35					40					
Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His	Leu	Ala	Ser	Pro	Glu				
			45					50					55						
Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys	Ser	Asp	Gly	Val	His	Thr				
		60					65					70							
Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met	Phe	Cys	Phe	Asp	Asn	Thr	Phe				
		75				80					85								
Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile	Phe	Phe	Glu	Leu	Ile	Pro	Asp	Asn				
90					95					100					105				
Met	Gly	Glu	Gln	Ala	Gln	Glu	Gln	Glu	Asp	Trp	Lys	Lys	Tyr	Ile	Thr				
				110					115					120					
Gly	Thr	Asp	Ile	Leu	Asp	Met	Lys	Leu	Glu	Asp	Ile	Leu	Val	Ser	Met				
			125					130					135						

Val Phe

<210> 150
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 150
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 -20 -15 -10
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 -5 1 5
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 10 15 20 25
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 30 35 40
 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 45 50 55
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 60 65 70
 Cys Ile Arg Ser Lys Asn Gly Pro Gly Thr Ala Val His Ala Tyr Asn
 75 80 85
 Pro Ser Thr Phe Arg Gly Gln Val
 90 95

<210> 151
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 151
 Met Val Glu Met Thr Gly Val
 1 5

<210> 152
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 152
 Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
 -40 -35 -30
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
 -25 -20 -15

Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
 -10 -5 1 5
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
 10 15 20
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
 25 30 35
 Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
 40 45 50
 Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
 55 60 65 70
 Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
 75 80 85
 Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
 90 95 100
 Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
 105 110 115
 Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Val Leu Ala
 120 125 130
 Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 135 140 145 150
 Gly Leu Lys Arg Lys Ala Glu
 155

<210> 153

<211> 43

<212> PRT

<213> Homo sapiens

<400> 153

Met Pro Phe Arg Met Ser Gly Tyr Ile Pro Phe Gly Thr Pro Ile Val
 5 10 15
 Ser Val Thr Phe Lys Gly Phe Pro Phe Leu Lys Asn Tyr Phe Lys Cys
 20 25 30
 Leu Thr Leu Cys Tyr Cys Ser Arg Val Phe Asp
 35 40

<210> 154

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 154

Met Glu Trp Ala Gly Lys Gln Arg Asp Phe Gln Val Arg Ala Ala Pro
 -35 -30 -25
 Gly Trp Asp His Leu Ala Ser Phe Pro Gly Pro Ser Leu Arg Leu Phe
 -20 -15 -10
 Ser Gly Ser Gln Ala Ser Val Cys Ser Leu Cys Ser Gly Phe Gly Ala
 -5 1 5 10
 Gln Glu

<210> 155
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 155
 Thr Val Pro Leu Leu Leu Glu Pro Ala Asp His Ala Arg Gly Arg Ala
 1 5 10 15
 His Val His Leu Pro Glu Asn Val Arg Ser Gln Ser Pro Gly His Val
 20 25 30
 Arg Arg Gly Arg Ser Gly Ala Gln Val Leu Pro Thr Gly Pro Asp Glu
 35 40 45
 Lys Gln Val Glu Lys Ser Glu Val Asp Phe Ser Lys Ser His Ser Leu
 50 55 60
 Val Arg Arg Phe Glu Asp Leu Lys Pro Lys Leu Ser Val Cys Lys Thr
 65 70 75 80
 Gly Ser Gln Val Phe Arg Ser Glu Asn Trp Lys Val Trp Ala Glu Ser
 85 90 95
 Ser Arg Gly Asp His Asp Asp Cys Leu Asp Leu Cys Ser Val Leu Cys
 100 105 110
 Trp Gly Glu Leu Leu Arg Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly
 115 120 125
 Glu Leu Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro
 130 135 140
 Gln Val Ser Gln Gln Glu Glu Leu Lys
 145 150

<210> 156
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 156
 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Lys Leu Met Met
 1 5 10 15
 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 20 25 30
 Gly Lys Asp Ile Asp Leu Asn Lys Val Arg Thr Lys Thr Ala Ala Lys
 35 40 45
 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val
 50 55 60
 Pro Pro Glu
 65

<210> 157
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 157

```

Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala Arg
1          5          10          15
Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val Ala Glu Val Phe
          20          25          30
Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu Thr Ile Lys Gly
          35          40          45
Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu Pro Glu Gln Ala
          50          55          60
Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala Lys Ala Asp Lys
65          70          75          80
Leu Ala Glu Glu His Ser Ser
          85

```

<210> 158

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -85...-1

<400> 158

```

Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
-85          -80          -75          -70
Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
          -65          -60          -55
Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
          -50          -45          -40
Met Pro Asn Val Arg Glu Leu Xaa Ala Arg Asn Leu Pro Pro Leu Thr
          -35          -30          -25
Glu Ala Gln Lys Asn Lys Leu Arg His Leu Ser Val Val Thr Leu Ala
          -20          -15          -10
Ala Lys Val Lys Cys Ile Pro Tyr Ala Val Leu Leu Glu Ala Leu Ala
5          1          5          10
Leu Arg Asn Val Arg Gln Leu Glu Asp Leu Val Ile Glu Ala Val Tyr
          15          20          25
Ala Asp Val Leu Arg Gly Ser Leu Asp Gln Arg Asn Gln Arg Leu Glu
          30          35          40
Val Asp Tyr Ser Ile Gly Arg Asp Ile Gln Arg Gln Asp Leu Ser Ala
          45          50          55
Ile Ala Arg Thr Leu Gln Glu Trp Cys Val Gly Cys Glu Val Val Leu
60          65          70          75
Ser Gly Ile Glu Glu Gln Val Ser Arg Ala Asn Gln His Lys Glu Gln
          80          85          90
Gln Leu Gly Leu Lys Gln Gln Ile Glu Ser Glu Val Ala Asn Leu Lys
          95          100          105
Lys Thr Ile Lys Val Thr Thr Ala Ala Ala Ala Ala Thr Ser Gln
          110          115          120
Asp Pro Glu Gln His Leu Thr Glu Leu Arg Glu Pro Ala Pro Gly Thr
          125          130          135
Asn Gln Arg Gln Pro Ser Lys Lys Ala Ser Lys Gly Lys Gly Leu Arg
140          145          150          155
Gly Ser Ala Lys Ile Trp Ser Lys Ser Asn
          160          165

```


<210> 159
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 159
 Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
 1 5 10 15
 His Ile Asn Ile Ser Phe His Arg
 20

<210> 160
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Pro Thr Asn Cys Ala Ala Ala Gly Cys Ala Thr Thr Tyr Asn Lys
 1 5 10 15
 His Ile Asn Ile Ser Phe His Arg Phe Pro Leu Asp Pro Lys Arg Arg
 20 25 30
 Lys Glu Trp Val Arg Leu Val Arg Arg Lys Asn Phe Val Pro Gly Lys
 35 40 45
 His Thr Phe Leu Cys Ser Lys His Phe Glu Ala Ser Cys Phe Asp Leu
 50 55 60
 Thr Gly Gln Thr Arg Arg Leu Lys Met Asp Ala Val Pro Thr Ile Phe
 65 70 75 80
 Asp Phe Cys Thr His Ile Lys Ser Met Lys Leu Lys Ser Arg Asn Leu
 85 90 95
 Leu Lys Lys Asn Asn Ser Cys Ser Pro Ala Gly Pro Ser Ser Leu Lys
 100 105 110
 Ser Asn Ile Ser Ser Gln Gln Val Leu Leu Glu His Ser Tyr Ala Phe
 115 120 125
 Arg Asn Pro Met Glu Ala Lys Lys Arg Ile Ile Lys Leu Glu Lys Glu
 130 135 140
 Ile Ala Ser Leu Arg Arg Lys Met Lys Thr Cys Leu Gln Lys Glu Arg
 145 150 155 160
 Arg Ala Thr Arg Arg Trp Ile Lys Ala Met Cys Leu Val Lys Asn Leu
 165 170 175
 Glu Ala Asn Ser Val Leu Pro Lys Gly Thr Ser Glu His Met Leu Pro
 180 185 190
 Thr Ala Leu Ser Ser Leu Pro Leu Glu Asp Phe Lys Ile Leu Glu Gln
 195 200 205
 Asp Gln Gln Asp Lys Thr Leu Leu Ser Leu Asn Leu Lys Gln Thr Lys
 210 215 220
 Ser Thr Phe Ile
 225

<210> 161
 <211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 161

```

Met Asn Leu His Phe Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly
-20          -15          -10          -5
Leu Val Leu Ala Pro Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe
          1          5          10
Pro Cys Ile Tyr Cys Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala
          15          20          25
Phe Ser Phe Ile Thr Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu
          30          35          40
Ile Leu Pro Glu Lys Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly
45          50          55          60
Pro Ala Lys Leu Arg Gln
          65

```

<210> 162

<211> 44

<212> PRT

<213> Homo sapiens

<400> 162

```

Met Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn
1          5          10          15
Pro Arg Leu Pro Gly Ser Ser Tyr Ser Pro Ala Ser Ala Thr Trp Val
          20          25          30
Arg Gly Ser Leu Glu Pro Gly Arg Leu Arg Leu Gln
          35          40

```

<210> 163

<211> 314

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -58..-1

<400> 163

```

Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val Ala
          -55          -50          -45
Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Arg Glu Thr Gly
          -40          -35          -30
Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val His
          -25          -20          -15
His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val Lys
-10          -5          1          5
Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr Lys Asn Val Pro

```

[illegible]

211> 89

212> PRT

<213> Hom

74

<221> SIG

<222> -80

Met Arg T

-80

Pro Arg A

Thr Ser C

Leu Cys G

Gln Lev G

Ser Thr G

1

5

<210> 165
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 165
 Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
 -15 -10 -5 1
 Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
 5 10 15
 Gln Gly Gly Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
 20 25 30
 His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
 35 40 45
 Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Val Phe
 50 55 60 65
 Arg Arg Glu Leu Ser Glu Tyr Thr Glu Gly Leu Thr Ser Glu Pro Leu
 70 75 80
 Thr Ala

<210> 166
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 166
 Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn
 -35 -30 -25
 Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly
 -20 -15 -10 -5
 Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe
 1 5 10
 His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His
 15 20 25
 Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly
 30 35 40
 Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 45 50 55

<210> 167
 <211> 351
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 167

Met	Val	Pro	Phe	Ile	Tyr	Leu	Gln	Ala	His	Phe	Thr	Leu	Cys	Ser	Gly
	-15					-10					-5				
Trp	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr
1				5					10					15	
Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile
			20					25					30		
Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr
		35					40					45			
Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu
	50					55					60				
Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Pro	Glu	Pro
65					70					75					80
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser
				85					90					95	
Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
			100					105					110		
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
		115					120					125			
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
	130					135					140				
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
145					150					155					160
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
				165					170					175	
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
		180						185					190		
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
	195						200					205			
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
	210					215					220				
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
225					230					235					240
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
				245					250					255	
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
			260					265					270		
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val
		275					280					285			
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys
	290					295					300				
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Cys
305					310					315					320
His	Leu	Gly	His	Gly	Arg	Leu	Trp	Leu	Gln	His	Ser	Thr	Asp	Arg	
				325					330					335	

<210> 168
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
<221> SIGNAL
<222> -47...-1

<400> 168

Met	Glu	Lys	Phe	Val	Asp	Pro	Gly	Asn	His	Asn	Ser	Gly	Ile	Asp	Leu
		-45					-40					-35			
Leu	Arg	Thr	Tyr	Leu	Trp	Arg	Cys	Gln	Phe	Leu	Leu	Pro	Phe	Val	Ser
	-30					-25					-20				
Leu	Gly	Leu	Met	Cys	Phe	Gly	Ala	Leu	Ile	Gly	Leu	Cys	Ala	Cys	Ile
-15					-10					-5					1
Cys	Arg	Ser	Leu	Tyr	Pro	Thr	Ile	Ala	Thr	Gly	Ile	Leu	His	Leu	Leu
		5					10						15		
Ala	Gly	Leu	Cys	Thr	Leu	Gly	Ser	Val	Ser	Cys	Tyr	Val	Ala	Gly	Ile
	20					25						30			
Glu	Leu	Leu	His	Gln	Lys	Leu	Glu	Leu	Pro	Asp	Asn	Val	Ser	Gly	Glu
	35					40					45				
Phe	Gly	Trp	Ser	Phe	Cys	Leu	Ala	Cys	Val	Ser	Ala	Pro	Leu	Gln	Phe
50					55					60					65
Met	Ala	Ser	Ala	Leu	Phe	Ile	Trp	Ala	Ala	His	Thr	Asn	Arg	Arg	Glu
				70					75					80	
Tyr	Thr	Leu	Met	Lys	Ala	Tyr	Arg	Val	Ala						
			85					90							

<210> 169
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -73...-1

<400> 169

Met	Asn	Leu	Glu	Arg	Val	Ser	Asn	Glu	Glu	Lys	Leu	Asn	Leu	Cys	Arg
		-70						-65					-60		
Lys	Tyr	Tyr	Leu	Gly	Gly	Phe	Ala	Phe	Leu	Pro	Phe	Leu	Trp	Leu	Val
	-55					-50						-45			
Asn	Ile	Phe	Trp	Phe	Tyr	Arg	Glu	Ala	Phe	Leu	Val	Pro	Ala	Tyr	Thr
	-40					-35					-30				
Glu	Gln	Ser	Gln	Ile	Lys	Gly	Tyr	Val	Trp	Arg	Ser	Ala	Val	Gly	Phe
-25					-20					-15				-10	
Leu	Phe	Trp	Val	Ile	Val	Leu	Thr	Ser	Trp	Ile	Thr	Ile	Phe	Gln	Ile
			-5					1				5			
Tyr	Arg	Pro	Arg	Trp	Gly	Ala	Leu	Gly	Asp	Tyr	Leu	Ser	Phe	Thr	Ile
	10					15						20			
Pro	Leu	Gly	Thr	Pro											
	25														

<210> 170
<211> 252
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68..-1

<400> 170

```

Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65                      -60                      -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50                      -45                      -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser
      -35                      -30                      -25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro
      -20                      -15                      -10                      -5
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly
      1                      5                      10
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His
      15                      20                      25
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu
      30                      35                      40
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys
      45                      50                      55                      60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe
      65                      70                      75
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro
      80                      85                      90
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn
      95                      100                      105
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu
      110                      115                      120
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro
      125                      130                      135                      140
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp
      145                      150                      155
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly
      160                      165                      170
Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys
      175                      180

```

<210> 171

<211> 350

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68..-1

<400> 171

```

Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu
      -65                      -60                      -55
Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val
      -50                      -45                      -40
Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser

```

-35						-30						-25			
Ala	Ser	Ala	Arg	Gly	Lys	Glu	Leu	Arg	Leu	Ile	Leu	Ser	Pro	Leu	Pro
-20					-15					-10					-5
Gly	Ala	Gln	Pro	Gln	Gln	Glu	Pro	Leu	Ala	Leu	Val	Phe	Arg	Phe	Gly
				1				5				10			
Met	Ser	Gly	Ser	Phe	Gln	Leu	Val	Pro	Arg	Glu	Glu	Leu	Pro	Arg	His
	15						20					25			
Ala	His	Leu	Arg	Phe	Tyr	Thr	Ala	Pro	Pro	Gly	Pro	Arg	Leu	Ala	Leu
	30					35					40				
Cys	Phe	Val	Asp	Ile	Arg	Arg	Phe	Gly	Arg	Trp	Asp	Leu	Gly	Gly	Lys
45					50					55					60
Trp	Gln	Pro	Gly	Arg	Gly	Pro	Cys	Val	Leu	Gln	Glu	Tyr	Gln	Gln	Phe
				65					70					75	
Arg	Leu	Lys	Ile	Pro	Pro	Phe	Glu	Lys	Ala	Arg	Ser	Val	Leu	Glu	Ala
			80					85					90		
Leu	Gln	Gln	His	Arg	Pro	Ser	Pro	Glu	Leu	Thr	Leu	Ser	Gln	Lys	Ile
	95						100					105			
Arg	Thr	Lys	Leu	Gln	Asn	Pro	Asp	Leu	Leu	Glu	Leu	Cys	His	Ser	Val
	110				115						120				
Pro	Lys	Glu	Val	Asp	Gln	Leu	Gly	Gly	Arg	Gly	Tyr	Gly	Ser	Glu	Ser
125					130					135					140
Gly	Glu	Glu	Asp	Phe	Ala	Ala	Phe	Arg	Ala	Trp	Leu	Arg	Cys	Tyr	Gly
				145					150					155	
Met	Pro	Gly	Met	Ser	Ser	Leu	Gln	Asp	Arg	His	Gly	Arg	Thr	Ile	Trp
			160					165					170		
Phe	Gln	Gly	Asp	Pro	Gly	Pro	Leu	Ala	Pro	Lys	Gly	Arg	Lys	Ser	Arg
	175						180					185			
Lys	Lys	Lys	Ser	Lys	Ala	Thr	Gln	Leu	Ser	Pro	Glu	Asp	Arg	Val	Glu
	190					195					200				
Asp	Ala	Leu	Pro	Pro	Ser	Lys	Ala	Pro	Ser	Lys	Thr	Arg	Arg	Ala	Lys
205					210					215					220
Arg	Asp	Leu	Pro	Lys	Arg	Thr	Ala	Thr	Gln	Arg	Pro	Glu	Gly	Thr	Ser
				225					230					235	
Leu	Gln	Gln	Asp	Pro	Glu	Ala	Pro	Thr	Val	Pro	Lys	Lys	Gly	Arg	Arg
			240					245					250		
Lys	Gly	Arg	Gln	Ala	Ala	Ser	Gly	His	Cys	Arg	Pro	Arg	Lys	Val	Lys
	255						260				265				
Ala	Asp	Ile	Pro	Ser	Leu	Glu	Pro	Glu	Gly	Thr	Ser	Ala	Ser		
	270					275					280				

<210> 172

<211> 390

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68..-1

<400> 172

Met	Pro	Glu	Gly	Pro	Glu	Leu	His	Leu	Ala	Ser	Gln	Phe	Val	Asn	Glu
			-65					-60				-55			
Ala	Cys	Arg	Ala	Leu	Val	Phe	Gly	Cys	Val	Glu	Lys	Ser	Ser	Val	
	-50					-45				-40					
Ser	Arg	Asn	Pro	Glu	Val	Pro	Phe	Glu	Ser	Ser	Ala	Tyr	Arg	Ile	Ser

-35		-30		-25
Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro				
-20		-15		-10
Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly				-5
	1	5	10	
Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His				
15	20	25		
Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu				
30	35	40		
Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys				
45	50	55		60
Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe				
	65	70		75
Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro				
	80	85		90
Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn				
95	100	105		
Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu				
110	115	120		
Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro				
125	130	135		140
Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp				
	145	150		155
Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly				
	160	165		170
Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe				
	175	180		185
Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln				
	190	195		200
Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu				
205	210	215		220
Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Ser Lys Ala Thr Gln				
	225	230		235
Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala				
	240	245		250
Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala				
	255	260		265
Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro				
	270	275		280
Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly				
285	290	295		300
His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro				
	305	310		315
Glu Gly Thr Ser Ala Ser				
	320			

<210> 173

<211> 190

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -82...-1

<400> 173

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Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
      -80                      -75                      -70
His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
      -65                      -60                      -55
Val Ser Leu Pro Gly Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile
      -50                      -45                      -40                      -35
Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
                        -30                      -25                      -20
Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr
                        -15                      -10                      -5
Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile
      1                      5                      10
Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile
      15                      20                      25                      30
Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu
                        35                      40                      45
Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu
                        50                      55                      60
Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe
                        65                      70                      75
Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His
      80                      85                      90
Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu
      95                      100                      105

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<210> 174

<211> 285

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -232..-1

<400> 174

```

Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile
      -230                      -225                      -220
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
      -215                      -210                      -205
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
      -200                      -195                      -190                      -185
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu
                        -180                      -175                      -170
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
                        -165                      -160                      -155
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
                        -150                      -145                      -140
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile
      -135                      -130                      -125
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys
      -120                      -115                      -110                      -105
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe
                        -100                      -95                      -90
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp

```

			-85					-80					-75			
Gly	His	Phe	Gln	Asn	Arg	Val	Asn	Leu	Val	Gly	Asp	Ile	Phe	Arg	Asn	
		-70					-65				-60					
Asp	Gly	Ser	Ile	Met	Leu	Gln	Gly	Val	Arg	Glu	Ser	Asp	Gly	Gly	Asn	
	-55					-50				-45						
Tyr	Thr	Cys	Ser	Ile	His	Leu	Gly	Asn	Leu	Val	Phe	Lys	Lys	Thr	Ile	
-40					-35					-30					-25	
Val	Leu	His	Val	Ser	Pro	Glu	Glu	Pro	Arg	Thr	Leu	Val	Thr	Pro	Ala	
			-20						-15					-10		
Ala	Leu	Arg	Pro	Leu	Val	Leu	Gly	Gly	Asn	Gln	Leu	Val	Ile	Ile	Val	
		-5					1			5						
Gly	Ile	Val	Cys	Ala	Thr	Ile	Leu	Leu	Leu	Pro	Val	Leu	Ile	Leu	Ile	
10						15				20						
Val	Lys	Lys	Thr	Cys	Gly	Asn	Lys	Ser	Ser	Val	Asn	Ser	Thr	Val	Leu	
25					30					35					40	
Val	Lys	Asn	Thr	Lys	Lys	Thr	Asn	Pro	Lys	Lys	Lys	Lys				
			45						50							

<210> 175

<211> 153

<212> PRT

<213> Homo sapiens

<400> 175

Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Val	Asp	Lys	Cys	Ile	Phe	Lys	Ile	
			5					10				15				
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu	
		20					25					30				
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg	
	35					40					45					
Val	His	Leu	Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu	
	50				55					60						
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg	
65				70				75						80		
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val	
			85					90					95			
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu	Ile	
		100						105					110			
Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val	Thr	Lys	
		115					120					125				
Val	Glu	Trp	Ile	Phe	Ser	Gly	Arg	Arg	Ala	Lys	Val	Thr	Arg	Arg	Lys	
	130					135					140					
His	His	Cys	Val	Arg	Glu	Gly	Ser	Gly								
145						150										

<210> 176

<211> 49

<212> PRT

<213> Homo sapiens

<400> 176

Met	Leu	Xaa	Gly	Asp	His	Arg	Ala	Leu	Leu	Leu	Lys	Ile	Trp	Leu	Leu	
1			5					10					15			

Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
 20 25 30
 Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe
 35 40 45
 Cys

<210> 177
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 177
 Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys
 -20 -15 -10
 Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys
 -5 1 5
 Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly
 10 15 20
 Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys
 25 30 35 40
 Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn
 45 50 55
 Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys
 60 65 70
 Pro Pro Arg
 75

<210> 178
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 178
 Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro
 -35 -30 -25
 Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Leu Asp Ala Leu Leu
 -20 -15 -10
 Arg Leu Gly Asp Thr Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys
 -5 1 5 10
 Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro
 15 20 25
 Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser
 30 35 40
 Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile
 45 50 55

<210> 179
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 179
Met Met Leu Pro Gln Trp Leu Leu Leu Leu Phe Leu Leu Phe Phe Phe
 -20 -15 -10
Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
 -5 1 5
Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
10 15 20 25
Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
 30 35 40
Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
 45 50 55
Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
 60 65 70
Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
 75 80 85
Gln Lys Leu Ala Lys Lys Met Phe Phe
90 95

<210> 180
<211> 59
<212> PRT
<213> Homo sapiens

<400> 180
Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
1 5 10 15
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 20 25 30
Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Glu Arg Thr Lys Tyr Glu
 35 40 45
Thr Pro Arg Lys Arg Glu Gly Lys Lys Lys Lys
50 55

<210> 181
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 181

```

Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys
      -10                      -5                      1
Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala
      5                      10                      15
Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp
      20                      25                      30
Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu
      35                      40                      45                      50
Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly
      55                      60                      65
Tyr Arg Ile Cys Asp Leu
      70

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<210> 182

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -58...-1

<400> 182

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Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile
      -55                      -50                      -45
Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro
      -40                      -35                      -30
Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu
      -25                      -20                      -15
Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val
      10                      -5                      1                      5
Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu
      10                      15                      20
Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg
      25                      30                      35
Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly
      40                      45                      50
Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu
      55                      60                      65                      70
Ser Leu Gln Asp Ala Leu Leu Leu Leu Leu Met Gly Leu Gly Pro Leu
      75                      80                      85
Leu Arg Ala Cys Gly Met Pro Leu Thr Leu Leu Gly Leu Ala Phe Cys
      90                      95                      100
Leu His Pro Trp Ala
      105

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<210> 183

<211> 80

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 183

Met	Pro	Phe	Gln	Phe	Gly	Thr	Gln	Pro	Arg	Arg	Phe	Pro	Val	Glu	Gly
-35					-30					-25					-20
Gly	Asp	Ser	Ser	Ile	Glu	Leu	Glu	Pro	Gly	Leu	Ser	Ser	Ser	Ala	Ala
			-15						-10					-5	
Cys	Asn	Gly	Lys	Glu	Met	Ser	Pro	Thr	Arg	Gln	Leu	Arg	Arg	Cys	Pro
		1				5					10				
Gly	Ser	His	Cys	Leu	Thr	Ile	Thr	Asp	Val	Pro	Val	Thr	Val	Tyr	Ala
15					20					25					
Thr	Thr	Arg	Lys	Pro	Pro	Ala	Gln	Ser	Ser	Lys	Glu	Met	His	Pro	Lys
30					35					40					45

<210> 184
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 184

Met	Ala	Pro	Gln	Thr	Leu	Leu	Pro	Val	Leu	Val	Leu	Cys	Val	Leu	Leu
-20					-15					-10					
Leu	Gln	Ala	Gln	Gly	Gly	Tyr	Arg	Asp	Lys	Met	Arg	Met	Gln	Arg	Ile
-5				1				5					10		
Lys	Val	Cys	Glu	Lys	Arg	Pro	Ser	Ile	Asp	Leu	Cys	Ile	His	His	Cys
		15					20					25			
Ser	Cys	Phe	Gln	Lys	Cys	Glu	Thr	Asn	Lys	Ile	Cys	Cys	Ser	Ala	Phe
		30					35					40			
Cys	Gly	Asn	Ile	Cys	Met	Ser	Ile	Leu							
45						50									

<210> 185
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 185

Met	Leu	Gly	Ala	Glu	Thr	Glu	Glu	Lys	Leu	Phe	Asp	Ala	Pro	Leu	Ser
1			5					10					15		
Ile	Ser	Lys	Arg	Glu	Gln	Leu	Glu	Gln	Gln	Val	Pro	Glu	Asn	Tyr	Phe
		20					25					30			
Tyr	Val	Pro	Asp	Leu	Gly	Gln	Val	Pro	Glu	Ile	Asp	Val	Pro	Ser	Tyr
	35					40					45				
Leu	Pro	Asp	Leu	Pro	Gly	Ile	Ala	Asn	Asp	Leu	Met	Tyr	Ile	Ala	Asp
50					55					60					
Leu	Gly	Pro	Gly	Ile	Ala	Pro	Ser	Ala	Pro	Gly	Thr	Ile	Pro	Glu	Leu
65				70					75						80

Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met
85 90 95
Gly Tyr

<210> 186
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 186
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu
-20 -15 -10
Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val
-5 1 5 10
Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val
15 20 25
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro
30 35 40
Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys
45 50 55
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr
60 65 70 75
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg
80 85 90

<210> 187
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 187
Met Cys Cys Tyr Cys Arg Ile Phe Cys Leu Arg Cys Thr Tyr Phe Pro
-40 -35 -30
Val His Cys Gly Met Cys Asn Leu Arg Tyr Phe Glu Phe Ser Thr Phe
-25 -20 -15
Leu Leu Ser Leu Ser Leu Ile Thr Tyr Cys Phe Trp Asp Pro Pro His
-10 -5 1
Arg Gly Ser His Ser Leu Ser Leu Glu His Thr Pro Leu Asp Phe Leu
5 10 15 20
Glu Trp Gly Leu Leu Arg
25

<210> 188

<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 188
Met Leu Phe Ser Leu Ser Leu Leu Ser Asn Leu Asn Gln Ile Gly Ser
 -10 -5 1
Ser His Leu Asp Arg Pro His Ile Pro Gly Gln Ser Ala Gln Leu Phe
 5 10 15
Ile Tyr Gln Met Ser Ser Gln Gln Leu Gln Gln Gln Pro Ser Ala Asn
20 25 30 35
Lys Lys Ala Gly Lys Ile His Asn Thr Pro Phe Ala Asn Gln Leu Asn
 40 45 50
Pro Thr Gln His Leu Ala Lys Pro Phe Gln Gln Ile Leu Pro Gly Arg
 55 60 65
Gln Ser Gly Ser Leu Thr Ser Pro Phe Leu Ala Cys
 70 75

<210> 189
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 189
Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
-10 -5 1 5
Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20
Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
 25 30 35
Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
 40 45 50
Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu
55 60 65 70
Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile
 75 80 85
Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu
 90 95 100
Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys
 105 110 115
Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro
 120 125 130
Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu

135		140		145		150								
Ala	Asp	Asp	Leu	Glu	Lys	Asn	Phe	Pro	Ser	Leu	Lys	Val	Gln	Thr
		155							160					165

<210> 190
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 190															
Met	Gln	Val	Ala	Leu	Lys	Glu	Asp	Leu	Asp	Ala	Leu	Lys	Glu	Lys	Phe
1				5					10					15	
Arg	Thr	Met	Glu	Ser	Asn	Gln	Lys	Ser	Ser	Phe	Gln	Glu	Ile	Pro	Lys
			20					25					30		
Leu	Asn	Glu	Glu	Leu	Leu	Ser	Lys	Gln	Lys	Gln	Leu	Glu	Lys	Ile	Glu
		35					40					45			
Ser	Gly	Glu	Met	Gly	Leu	Asn	Lys	Val	Trp	Ile	Asn	Ile	Thr	Glu	Met
	50					55					60				
Asn	Lys	Gln	Ile	Ser	Leu	Leu	Thr	Ser	Ala	Val	Asn	His	Leu	Lys	Ala
65					70				75						80
Asn	Val	Lys	Ser	Ala	Ala	Asp	Leu	Ile	Ser	Leu	Pro	Thr	Thr	Val	Glu
				85					90					95	
Gly	Leu	Gln	Lys	Ser	Val	Ala	Ser	Ile	Gly	Asn	Thr	Leu	Asn	Ser	Val
			100					105					110		
His	Leu	Ala	Val	Glu	Ala	Leu	Gln	Lys	Thr	Val	Asp	Glu	His	Lys	Lys
		115					120					125			
Thr	Met	Glu	Leu	Leu	Gln	Ser	Asp	Met	Asn	Gln	His	Phe	Leu	Lys	Glu
	130					135					140				
Thr	Pro	Gly	Ser	Asn	Gln	Ile	Ile	Pro	Ser	Pro	Ser	Ala	Thr	Ser	Glu
145					150					155					160
Leu	Asp	Asn	Lys	Thr	His	Ser	Glu	Asn	Leu	Lys	Gln	Met	Gly	Asp	Arg
			165					170						175	
Ser	Ala	Thr	Leu	Lys	Arg	Gln	Ser	Leu	Asp	Gln	Val	Thr	Asn	Arg	Thr
			180					185					190		
Asp	Thr	Val	Lys	Ile	Gln	Lys	Lys								
		195				200									

<210> 191
 <211> 379
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 191															
Met	Pro	His	Ser	Ser	Leu	His	Pro	Ser	Ile	Pro	Cys	Pro	Arg	Gly	His
		-35					-30					-25			
Gly	Ala	Gln	Lys	Ala	Ala	Leu	Val	Leu	Leu	Ser	Ala	Cys	Leu	Val	Thr
	-20					-15					-10				
Leu	Trp	Gly	Leu	Gly	Glu	Pro	Pro	Glu	His	Thr	Leu	Arg	Tyr	Leu	Val
-5					1				5					10	

```

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys
      15                20                25
Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser
      30                35                40
Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly
      45                50                55
Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala
      60                65                70                75
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln
      80                85                90
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile
      95                100               105
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala
     110               115               120
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln
     125               130               135
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly
     140               145               150               155
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val
     160               165               170
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys
     175               180               185
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr
     190               195               200
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr
     205               210               215
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser
     220               225               230               235
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala
     240               245               250
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu
     255               260               265
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp
     270               275               280
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu
     285               290               295
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro
     300               305               310               315
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Leu Ser Gly Met
     320               325               330
Gly Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
     335               340

```

<210> 192

<211> 112

<212> PRT

<213> Homo sapiens

<400> 192

```

Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
1      5                10                15
Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
      20                25                30
Glu Asp Val Leu Glu Glu Cys Met Ser Leu Pro Lys Leu Ser Ser Tyr
      35                40                45

```

Ser	Gly	Trp	Val	Val	Glu	His	Val	Leu	Pro	His	Met	Gln	Glu	Asn	Gln
50						55					60				
Pro	Leu	Ser	Glu	Thr	Ser	Pro	Ser	Ser	Thr	Ser	Ala	Ser	Ala	Leu	Asp
65					70				75					80	
Gln	Pro	Ser	Phe	Val	Pro	Lys	Ser	Pro	Asp	Ala	Ser	Ser	Ala	Phe	Ser
			85					90						95	
Pro	Ala	Ser	Pro	Ala	Thr	Pro	Asn	Gly	Thr	Lys	Gly	Lys	Lys	Lys	Lys
			100					105					110		

<210> 193
 <211> 43
 <212> PRT
 <213> Homo sapiens

Ser	Leu	Pro	Gln	Ala	Leu	Trp	Phe	Gln	Phe	Phe	Tyr	His	Ser	Gly	Ser
1			5					10						15	
Ser	Leu	Glu	Ser	Pro	Gly	Met	Leu	Asn	Gly	Pro	Phe	Gln	His	Arg	Asn
			20					25					30		
Ser	Arg	Ile	Met	Thr	His	Arg	Ser	Ala	Glu	Lys					
		35					40								

<210> 194
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

Met	Leu	Arg	Ile	Ala	Leu	Thr	Leu	Ile	Pro	Ser	Met	Leu	Ser	Arg	Ala
-15						-10					-5				
Ala	Gly	Trp	Cys	Trp	Tyr	Lys	Glu	Pro	Thr	Gln	Gln	Phe	Ser	Tyr	Leu
1			5					10						15	
Cys	Leu	Pro	Cys	Leu	Ser	Trp	Asn	Lys	Lys	Gly	Asn	Val	Leu	Gln	Leu
			20					25					30		
Pro	Asn	Phe													
		35													

<210> 195
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 195

```

Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala
      -15                      -10                      -5
Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser
      1                      5                      10
Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile
15                      20                      25                      30
Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys
      35                      40                      45
Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp
      50                      55                      60
Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly
      65                      70                      75
Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala
      80                      85                      90
Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe
95                      100                      105                      110
Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr
      115                      120                      125
Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro
      130                      135                      140
Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln
      145                      150                      155
Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp
160                      165                      170
Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro
175                      180                      185                      190
His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu Val
      195                      200                      205
Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly
      210                      215                      220
Arg Thr Ala Trp
      225

```

<210> 196

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<400> 196

```

Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
      -30                      -25                      -20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val
      -15                      -10                      -5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln
      1                      5                      10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp
15                      20                      25                      30
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn
      35                      40                      45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys
      50                      55                      60

```

[illegible]

הַיְּהוּדִים הָיוּ מְשֻׁלָּלִים בְּמִשְׁכַּנְּהֶם

100

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<400> 198

```

Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
      -45                      -40                      -35
Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
      -30                      -25                      -20
Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
      -15                      -10                      -5
Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
1      5      10      15
Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
      20      25      30
Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser
      35      40      45
Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
      50      55      60

```

<210> 199

<211> 54

<212> PRT

<213> Homo sapiens

<400> 199

```

Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr
      5      10      15
Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr
      20      25      30
Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln
      35      40      45
Ser Ser Gly His Leu Pro
      50

```

<210> 200

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 200

```

Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr Ala Ala Val
      -20                      -15                      -10
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
      -5      1      5      10
Lys Lys Gln Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
      15      20      25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
      30      35      40
Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Ile Thr Glu Glu Asp
      45      50      55
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val

```

60		65		70		75									
Lys	Glu	Tyr	Asp	Arg	Ala	Ala	His	Phe	Leu	His	Gly	Cys	Asn	Ser	Lys
			80					85					90		
Lys	Ala	Tyr	Phe	Leu	Tyr	Met	Tyr	Ser	Arg	Tyr	Leu	Val	Arg	Ala	Ile
		95						100					105		
Leu	Lys	Cys	His	Ser	Ala	Phe	Ser	Glu	Thr	Ser	Ile	Phe	Arg	Thr	Asn
		110					115					120			
Gly	Lys	Val	Lys	Ser	Phe	Lys									
	125					130									

<210> 201
 <211> 228
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 201

Met	Ser	Met	Ala	Val	Glu	Thr	Phe	Gly	Phe	Phe	Met	Ala	Thr	Val	Gly
-25					-20				-15						-10
Leu	Leu	Met	Leu	Gly	Val	Thr	Leu	Pro	Asn	Ser	Tyr	Trp	Arg	Val	Ser
			-5					1				5			
Thr	Val	His	Gly	Asn	Val	Ile	Thr	Thr	Asn	Thr	Ile	Phe	Glu	Asn	Leu
		10				15					20				
Trp	Phe	Ser	Cys	Ala	Thr	Asp	Ser	Leu	Gly	Val	Tyr	Asn	Cys	Trp	Glu
	25				30				35						
Phe	Pro	Ser	Met	Leu	Ala	Leu	Ser	Gly	Tyr	Ile	Gln	Ala	Cys	Arg	Ala
40				45					50						55
Leu	Met	Ile	Thr	Ala	Ile	Leu	Leu	Gly	Phe	Leu	Gly	Leu	Leu	Leu	Gly
			60					65					70		
Ile	Ala	Gly	Leu	Arg	Cys	Thr	Asn	Ile	Gly	Gly	Leu	Glu	Leu	Ser	Arg
		75					80					85			
Lys	Ala	Lys	Leu	Ala	Ala	Thr	Ala	Gly	Ala	Pro	His	Ile	Leu	Ala	Gly
	90					95					100				
Ile	Cys	Gly	Met	Val	Ala	Ile	Ser	Trp	Tyr	Ala	Phe	Asn	Ile	Thr	Arg
	105					110				115					
Asp	Phe	Phe	Asp	Pro	Leu	Tyr	Pro	Gly	Thr	Lys	Tyr	Glu	Leu	Gly	Pro
120					125					130					135
Ala	Leu	Tyr	Leu	Gly	Trp	Ser	Ala	Ser	Leu	Ile	Ser	Ile	Leu	Gly	Gly
			140						145					150	
Leu	Cys	Leu	Cys	Ser	Ala	Cys	Cys	Cys	Gly	Ser	Asp	Glu	Asp	Pro	Ala
		155					160					165			
Ala	Ser	Ala	Arg	Arg	Pro	Tyr	Gln	Ala	Pro	Val	Ser	Val	Met	Pro	Val
	170					175						180			
Ala	Thr	Ser	Asp	Gln	Glu	Gly	Asp	Ser	Ser	Phe	Gly	Lys	Tyr	Gly	Arg
	185					190					195				
Asn	Ala	Tyr	Val												
200															

<210> 202
 <211> 64

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 202
Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
-45 -40 -35
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
-30 -25 -20
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
-15 -10 -5 1
Pro Asp Leu Pro Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr
5 10 15

<210> 203
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 203
Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly
-30 -25 -20
Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile
15 -10 -5 1
Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys
5 10 15
Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu
20 25 30
Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn
35 40 45
Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile Pro Val Ser Gly Ser
50 55 60 65
Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg Gly Gly Pro Phe
70 75 80
Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu Lys Asp Gly Gln
85 90 95
Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly Asp Glu Val Lys
100 105 110
Lys Glu
115

<210> 204
<211> 87
<212> PRT
<213> Homo sapiens

<400> 204

```

Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser Leu
1          5          10          15
Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His Leu
          20          25          30
Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro Glu
          35          40          45
Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln Ser
          50          55          60
Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu Leu
65          70          75          80
Glu Val Asp Asp Trp Glu Phe
          85

```

<210> 205

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 205

```

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
          -25          -20          -15
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
          -10          -5          1          5
Leu Ser Leu Arg Ser Ala Met Ser
          10

```

<210> 206

<211> 154

<212> PRT

<213> Homo sapiens

<400> 206

```

Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg
1          5          10          15
Leu Cys Glu Arg Asp Val Ser Ser Ser Leu Arg Leu Thr Arg Ser Ser
          20          25          30
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro
          35          40          45
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr
          50          55          60
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu
65          70          75          80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys
          85          90          95
Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val
          100          105          110
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg
          115          120          125

```

His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys
 130 135 140
 Glu Glu Ala Ala Met Lys Ala Lys Thr Glu
 145 150

<210> 207
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 207
 Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
 1 5 10 15
 Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
 20 25 30
 Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
 35 40 45
 Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
 50 55 60
 Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
 65 70 75 80
 Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
 85 90 95
 Lys Gln Thr Ser Val
 100

<210> 208
 <211> 456
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 208
 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly
 -20 -15 -10
 Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn
 -5 1 5 10
 Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu
 15 20 25
 Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser
 30 35 40
 Glu Glu Glu Glu Glu Glu Arg Lys Lys Lys Cys Pro Lys Lys Ala Ser
 45 50 55
 Phe Ala Ser Ala Ser Ala Glu Val Gly Lys Lys Gly Lys Lys Lys Cys
 60 65 70
 Gln Lys Gln Gly Pro Pro Cys Ser Asp Ser Glu Glu Val Glu Arg
 75 80 85 90
 Lys Lys Lys Cys His Lys Gln Ala Leu Val Gly Ser Asp Ser Ala Glu
 95 100 105
 Asp Glu Lys Arg Lys Arg Lys Cys Gln Lys His Ala Pro Ile Asn Ser

			110					115					120				
Ala	Gln	His	Leu	Asp	Asn	Val	Asp	Gln	Thr	Gly	Pro	Lys	Ala	Trp	Lys		
			125					130					135				
Gly	Ser	Thr	Thr	Asn	Asp	Pro	Pro	Lys	Gln	Ser	Pro	Gly	Ser	Thr	Ser		
			140					145					150				
Pro	Lys	Pro	Pro	His	Thr	Leu	Ser	Arg	Lys	Gln	Trp	Arg	Asn	Arg	Gln		
						160				165					170		
Lys	Asn	Lys	Arg	Arg	Cys	Lys	Asn	Lys	Phe	Gln	Pro	Pro	Gln	Val	Pro		
					175					180					185		
Asp	Gln	Ala	Pro	Ala	Glu	Ala	Pro	Thr	Glu	Lys	Thr	Glu	Val	Ser	Pro		
			190						195				200				
Val	Pro	Arg	Thr	Asp	Ser	His	Gly	Ala	Arg	Ala	Gly	Ala	Leu	Arg	Ala		
			205					210					215				
Arg	Met	Ala	Gln	Arg	Leu	Asp	Gly	Ala	Arg	Phe	Arg	Tyr	Leu	Asn	Glu		
			220				225					230					
Gln	Leu	Tyr	Ser	Gly	Pro	Ser	Ser	Ala	Ala	Gln	Arg	Leu	Phe	Gln	Glu		
					240					245					250		
Asp	Pro	Glu	Ala	Phe	Leu	Leu	Tyr	His	Arg	Gly	Phe	Gln	Ser	Gln	Val		
					255					260					265		
Lys	Lys	Trp	Pro	Leu	Gln	Pro	Val	Asp	Arg	Ile	Ala	Arg	Asp	Leu	Arg		
			270					275					280				
Gln	Arg	Pro	Ala	Ser	Leu	Val	Val	Ala	Asp	Phe	Gly	Cys	Gly	Asp	Cys		
			285					290					295				
Arg	Leu	Ala	Ser	Ser	Ile	Arg	Asn	Pro	Val	His	Cys	Phe	Asp	Leu	Ala		
			300				305					310					
Ser	Leu	Asp	Pro	Arg	Val	Thr	Val	Cys	Asp	Met	Ala	Gln	Val	Pro	Leu		
			315				320				325				330		
Glu	Asp	Glu	Ser	Val	Asp	Val	Ala	Val	Phe	Cys	Leu	Ser	Leu	Met	Gly		
					335					340					345		
Thr	Asn	Ile	Arg	Asp	Phe	Leu	Glu	Glu	Ala	Asn	Arg	Val	Leu	Lys	Pro		
			350					355					360				
Gly	Gly	Leu	Leu	Lys	Val	Ala	Glu	Val	Ser	Ser	Arg	Phe	Glu	Asp	Val		
			365				370					375					
Arg	Thr	Phe	Leu	Arg	Ala	Val	Thr	Lys	Leu	Gly	Phe	Lys	Ile	Val	Ser		
			380				385				390						
Lys	Asp	Leu	Thr	Asn	Ser	His	Phe	Phe	Leu	Phe	Asp	Phe	Gln	Lys	Thr		
					400					405					410		
Gly	Pro	Pro	Leu	Val	Gly	Pro	Lys	Ala	Gln	Leu	Ser	Gly	Leu	Gln	Leu		
					415				420						425		
Gln	Pro	Cys	Leu	Tyr	Lys	Arg	Arg										
			430														

<210> 209

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 209

Met	Pro	Ser	Ser	Phe	Phe	Leu	Leu	Leu	Gln	Phe	Phe	Leu	Arg	Ile	Asp		
						-15			-10			-5					
Gly	Val	Leu	Ile	Arg	Met	Asn	Asp	Thr	Arg	Leu	Tyr	His	Glu	Ala	Asp		

1	5	10	15
Lys Thr Tyr Met	Leu Arg Glu Tyr Thr	Ser Arg Glu Ser	Lys Ile Ser
	20	25	30
Ser Leu Met His Val	Pro Pro Ser Leu Phe Thr	Glu Pro Asn Glu Ile	
	35	40	45
Ser Gln Tyr Leu Pro	Ile Lys Glu Ala Val Cys Glu	Lys Leu Ile Phe	
	50	55	60
Pro Glu Arg Ile Asp	Pro Asn Pro Ala Asp	Ser Gln Lys Ser Thr	Gln
	65	70	75
Val Glu			
80			

<210> 210
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 210
Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu
Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe
Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr
Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro
Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg
Asn Ala Ser

<210> 211
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 211
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

[illegible] $\langle 210 \rangle \quad 212$ $\langle 211 \rangle$ 152

1212> PRT

<213> Homo sapiens

220

<221> SIGNAL

$\langle 222 \rangle$ -21..-1

$\angle 400^\circ = 212$

Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys

-20 -15 -10

Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly

5	1	5	10
---	---	---	----

Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly

15 20 25

Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr

30 35 40

Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly

45 50 55

Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val

60 65 70 75

Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp
 80 85 90

80 85 90

Iug Ala Leu Ile Phe Arg Iug Ile His His Gly Leu Arg Gly Phe Cys

Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys
 85 100 105

Ser Val His Thr Leu Gly Gly Val Tyr Ile Gly Leu Phe Gly Leu Gly

See Val 115 111 200 011 010 010 010 010 111 110 010 200 110 011 010 010

Asn Asn Phe Ser Gln Glu Ser Ser

125 130

<210> 213
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 213

Met	Ala	Ala	Ser	Glu	Ala	Ala	Val	Val	Ser	Ser	Pro	Ser	Leu	Lys	Thr
				-50					-45					-40	
Asp	Thr	Ser	Pro	Val	Leu	Glu	Thr	Ala	Gly	Thr	Val	Ala	Ala	Met	Ala
			-35					-30					-25		
Ala	Thr	Pro	Ser	Ala	Arg	Ala	Ala	Ala	Ala	Val	Val	Ala	Ala	Ala	Ala
		-20				-15						-10			
Arg	Thr	Gly	Ser	Glu	Ala	Arg	Val	Ser	Lys	Ala	Ala	Leu	Ala	Thr	Lys
	-5				1				5					10	
Leu	Leu	Ser	Leu	Ser	Gly	Val	Phe	Ala	Val	His	Lys	Pro	Lys	Gly	Pro
			15					20					25		
Thr	Ser	Ala	Glu	Leu	Leu	Asn	Arg	Leu	Lys	Glu	Lys	Leu	Leu	Ala	Glu
			30					35					40		
Ala	Gly	Met	Pro	Ser	Pro	Glu	Trp	Thr	Lys	Arg	Lys	Lys	Gln	Thr	Leu
		45					50					55			
Lys	Ile	Gly	His	Gly	Gly	Thr	Leu	Asp	Ser	Ala	Ala	Arg	Gly	Val	Leu
	60					65				70					
Val	Val	Gly	Ile	Gly	Ser	Gly	Thr	Lys	Met	Leu	Thr	Ser	Met	Leu	Ser
	75				80					85				90	
Gly	Ser	Lys	Arg	Tyr	Thr	Ala	Ile	Gly	Glu	Leu	Gly	Lys	Ala	Thr	Asp
			95					100					105		
Thr	Leu	Asp	Ser	Thr	Gly	Lys	Val	Thr	Glu	Glu	Lys	Pro	Tyr	Gly	Met
			110					115					120		
Asn	Leu	Ile													
			125												

<210> 214
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -92..-1

<400> 214

Met	Ile	Thr	His	Val	Thr	Leu	Glu	Asp	Ala	Leu	Ser	Asn	Val	Asp	Leu
		-90					-85					-80			
Leu	Glu	Glu	Leu	Pro	Leu	Pro	Asp	Gln	Gln	Pro	Cys	Ile	Glu	Pro	Pro
	-75					-70					-65				
Pro	Ser	Ser	Ile	Met	Tyr	Gln	Ala	Asn	Phe	Asp	Thr	Asn	Phe	Glu	Asp
	-60			-55					-50					-45	
Arg	Asn	Ala	Phe	Val	Thr	Gly	Ile	Ala	Arg	Tyr	Ile	Glu	Gln	Ala	Thr
			-40					-35					-30		
Val	His	Ser	Ser	Met	Asn	Glu	Met	Leu	Glu	Glu	Gly	His	Glu	Tyr	Ala
			-25				-20						-15		

Val	Met	Leu	Tyr	Thr	Trp	Arg	Ser	Cys	Ser	Arg	Ala	Ile	Pro	Gln	Val
		-10					-5					1			
Lys	Cys	Asn	Glu	Gln	Pro	Asn	Arg	Val	Glu	Ile	Tyr	Glu	Lys	Thr	Val
5					10					15					20
Glu	Val	Leu	Glu	Pro	Glu	Val	Thr	Lys	Leu	Met	Lys	Phe	Met	Tyr	Phe
				25					30					35	
Gln	Arg	Lys	Ala	Ile	Glu	Arg	Phe	Cys	Ser	Glu	Val	Lys	Arg	Leu	Cys
			40					45					50		
His	Ala	Glu	Arg	Arg	Lys	Asp	Phe	Val	Ser	Glu	Ala	Tyr	Leu	Leu	Thr
		55					60					65			
Leu	Gly	Lys	Phe	Ile	Asn	Met	Phe	Ala	Val	Leu	Asp	Glu	Leu	Lys	Asn
		70				75					80				
Met	Lys	Cys	Ser	Val	Lys	Asn	Asp	His	Ser	Ala	Tyr	Lys	Arg	Ala	Ala
85					90					95					100
Gln	Phe	Leu	Arg	Lys	Met	Ala	Asp	Pro	Gln	Ser	Ile	Gln	Glu	Ser	Gln
				105					110					115	
Asn	Leu	Ser	Met	Phe	Leu	Ala	Asn	His	Asn	Arg	Ile	Thr	Gln	Cys	Leu
			120					125					130		
His	Gln	Gln	Leu	Glu	Val	Ile	Pro	Gly	Tyr	Glu	Glu	Leu	Leu	Ala	Asp
		135					140					145			
Ile	Val	Asn	Ile	Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Lys	Met	Tyr	Leu	Thr
	150					155					160				
Pro	Ser	Glu	Lys	His	Met	Leu	Lys	Val	Lys	Leu	Pro				
165					170					175					

$\angle 210^\circ$ 215

$\langle 211 \rangle$ 135

212> PRT

<213> Homo sapiens

 $\langle 220 \rangle$

¹¹
<221> SIGNAL

$$\langle 222 \rangle \quad -22, \dots, -1$$
$$K_{400} > 215$$
[illegible]

<210> 216
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 216
 Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 -35 -30 -25
 Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr
 -20 -15 -10
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 -5 1 5 10
 Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 15 20 25
 Glu Val Leu

<210> 217
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54...-1

<400> 217
 Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 -50 -45 -40
 Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
 -35 -30 -25
 Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
 -20 -15 -10
 Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
 -5 1 5 10
 Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
 15 20 25
 Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
 30 35 40
 Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
 45 50 55
 Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
 60 65 70

<210> 218
 <211> 376
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 218

Met	Gly	His	Arg	Phe	Leu	Arg	Gly	Leu	Leu	Thr	Leu	Leu	Leu	Pro	Pro
-20						-15				-10					
Pro	Pro	Leu	Tyr	Thr	Arg	His	Arg	Met	Leu	Gly	Pro	Glu	Ser	Val	Pro
-5					1			5						10	
Pro	Pro	Lys	Arg	Ser	Arg	Ser	Lys	Leu	Met	Ala	Pro	Pro	Arg	Ile	Gly
			15				20						25		
Thr	His	Asn	Gly	Thr	Phe	His	Cys	Asp	Glu	Ala	Leu	Ala	Cys	Ala	Leu
		30					35					40			
Leu	Arg	Leu	Leu	Pro	Glu	Tyr	Arg	Asp	Ala	Glu	Ile	Val	Arg	Thr	Arg
	45					50					55				
Asp	Pro	Glu	Lys	Leu	Ala	Ser	Cys	Asp	Ile	Val	Val	Asp	Val	Gly	Gly
60					65					70					75
Glu	Tyr	Asp	Pro	Arg	Arg	His	Arg	Tyr	Asp	His	His	Gln	Arg	Ser	Phe
				80					85					90	
Thr	Glu	Thr	Met	Ser	Ser	Leu	Ser	Pro	Gly	Arg	Pro	Trp	Gln	Thr	Lys
			95					100					105		
Leu	Ser	Ser	Ala	Gly	Leu	Ile	Tyr	Leu	His	Phe	Gly	His	Lys	Leu	Leu
			110				115					120			
Ala	Gln	Leu	Leu	Gly	Thr	Ser	Glu	Glu	Asp	Ser	Met	Val	Gly	Thr	Leu
			125				130					135			
Tyr	Asp	Lys	Met	Tyr	Glu	Asn	Phe	Val	Glu	Glu	Val	Asp	Ala	Val	Asp
140						145					150				155
Asn	Gly	Ile	Ser	Gln	Trp	Ala	Glu	Gly	Glu	Pro	Arg	Tyr	Ala	Leu	Thr
				160					165					170	
Thr	Thr	Leu	Ser	Ala	Arg	Val	Ala	Arg	Leu	Asn	Pro	Thr	Trp	Asn	His
			175					180					185		
Pro	Asp	Gln	Asp	Thr	Glu	Ala	Gly	Phe	Lys	Arg	Ala	Met	Asp	Leu	Val
		190					195					200			
Gln	Glu	Glu	Phe	Leu	Gln	Arg	Leu	Asp	Phe	Tyr	Gln	His	Ser	Trp	Leu
	205					210					215				
Pro	Ala	Arg	Ala	Leu	Val	Glu	Glu	Ala	Leu	Ala	Gln	Arg	Phe	Gln	Val
220					225					230					235
Asp	Pro	Ser	Gly	Glu	Ile	Val	Glu	Leu	Ala	Lys	Gly	Ala	Cys	Pro	Trp
				240					245					250	
Lys	Glu	His	Leu	Tyr	His	Leu	Glu	Ser	Gly	Leu	Ser	Pro	Pro	Val	Ala
			255					260					265		
Ile	Phe	Phe	Val	Ile	Tyr	Thr	Asp	Gln	Ala	Gly	Gln	Trp	Arg	Ile	Gln
		270					275					280			
Cys	Val	Pro	Lys	Glu	Pro	His	Ser	Phe	Gln	Ser	Arg	Leu	Pro	Leu	Pro
						290					295				
Glu	Pro	Trp	Arg	Gly	Leu	Arg	Asp	Glu	Ala	Leu	Asp	Gln	Val	Ser	Gly
300					305					310					315
Ile	Pro	Gly	Cys	Ile	Phe	Val	His	Ala	Ser	Gly	Phe	Ile	Gly	Gly	His
				320					325					330	
Arg	Thr	Arg	Glu	Gly	Ala	Leu	Ser	Met	Ala	Arg	Ala	Thr	Leu	Ala	Gln
			335					340					345		
Arg	Ser	Tyr	Leu	Pro	Gln	Ile	Ser								
		350				355									

<210> 219

<211> 211
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 219

```

Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
-30          -25          -20          -15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
          -10          -5          1
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
      5          10          15
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
  20          25          30
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 35          40          45          50
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
          55          60          65
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val Pro Arg Met
      70          75          80
Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe
      85          90          95
His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro
  100          105          110
Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser
 115          120          125          130
Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly
          135          140          145
Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser
          150          155          160
Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser
          165          170          175
Arg Gln Leu
  180

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<210> 220
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -60..-1

<400> 220

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Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu
-60          -55          -50          -45
Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys
          -40          -35          -30
Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu
          -25          -20          -15
Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln

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	-10						-5				1						
Cys	Trp	Trp	Arg	Thr	Leu	Val	Gln	Arg	Arg	Ile	Arg	Gln	Arg	Arg	Gln		
5					10					15					20		
Ala	Leu	Leu	Arg	Val	Tyr	Val	Ile	Gln	Glu	Gln	Ala	Thr	Val	Lys	Leu		
				25					30					35			
Gln	Ser	Cys	Ile	Arg	Met	Trp	Gln	Cys	Arg	Gln	Cys	Tyr	Arg	Gln	Met		
			40					45					50				
Cys	Asn	Ala	Leu	Cys	Leu	Phe	Gln	Val	Pro	Glu	Ser	Ser	Leu	Ala	Phe		
		55					60					65					
Gln	Thr	Asp	Gly	Phe	Leu	Gln	Val	Gln	Tyr	Ala	Ile	Pro	Ser	Lys	Gln		
	70					75					80						
Pro	Glu	Phe	His	Ile	Glu	Ile	Leu	Ser	Ile								
85						90											

<210> 221
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

Met	Lys	Gly	Gly	Ala	Phe	Ser	Asn	Leu	Asn	Asp	Ser	Gln	Leu	Ser	Ala		
		-40					-35					-30					
Ser	Phe	Leu	Gln	Pro	Ser	Leu	Gln	Ala	Asn	Cys	Pro	Ala	Leu	Asp	Pro		
	-25					-20				-15							
Ala	Val	Ser	Leu	Ser	Ala	Pro	Ala	Phe	Ala	Ser	Ala	Leu	Arg	Ser	Met		
-10					-5					1			5				
Lys	Ser	Ser	Gln	Ala	Ala	Arg	Lys	Asp	Asp	Phe	Leu	Arg	Ser	Leu	Ser		
		10					15					20					
Asp	Gly	Asp	Ser	Gly	Thr	Ser	Glu	His	Ile	Ser	Ala	Val	Val	Thr	Ser		
	25						30					35					
Pro	Arg	Ile	Ser	Cys	His	Gly	Ala	Ala	Ile	Pro	Thr	Ala	Arg	Ala	Leu		
	40					45					50						
Cys	Leu	Gly	Cys	Ser	Cys	Cys	Thr	Glu	Arg	Leu	Leu	Leu	Pro	Pro	Pro		
55					60					65					70		
Ser	Leu	Leu	Ser	Leu	Glu	Ala	Pro	Ala	Ser	Thr							
				75					80								

<210> 222
 <211> 346
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

Met	Ala	Met	Ala	Gln	Lys	Leu	Ser	His	Leu	Leu	Pro	Ser	Leu	Arg	Gln		
				-15					-10					-5			


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> 210> 224
<211> 184
<212> PRT
> 213> Homo sapiens
<220>
> 221> SIGNAL
> 222> -20..-1

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<400> 224																
Met	Asp	Asn	Arg	Phe	Ala	Thr	Ala	Phe	Val	Ile	Ala	Cys	Val	Leu	Ser	
-20					-15					-10					-5	
Leu	Ile	Ser	Thr	Ile	Tyr	Met	Ala	Ala	Ser	Ile	Gly	Thr	Asp	Phe	Trp	
				1				5					10			
Tyr	Glu	Tyr	Arg	Ser	Pro	Val	Gln	Glu	Asn	Ser	Ser	Asp	Leu	Asn	Lys	
		15					20					25				
Ser	Ile	Trp	Asp	Glu	Phe	Ile	Ser	Asp	Glu	Ala	Asp	Glu	Lys	Thr	Tyr	
	30					35					40					
Asn	Asp	Ala	Pro	Phe	Arg	Tyr	Asn	Gly	Thr	Val	Gly	Leu	Trp	Arg	Arg	
45					50					55					60	
Cys	Ile	Thr	Ile	Pro	Lys	Asn	Met	His	Trp	Tyr	Ser	Pro	Pro	Glu	Arg	
				65					70					75		
Thr	Glu	Ser	Phe	Asp	Val	Val	Thr	Lys	Cys	Val	Ser	Phe	Thr	Leu	Thr	
			80					85					90			
Glu	Gln	Phe	Met	Glu	Lys	Phe	Val	Asp	Pro	Gly	Asn	His	Asn	Ser	Gly	
		95					100					105				
Ile	Asp	Leu	Leu	Arg	Thr	Tyr	Leu	Trp	Arg	Cys	Gln	Phe	Leu	Leu	Pro	
	110					115					120					

Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys
 125 130 135 140
 Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu
 145 150 155
 His Leu Leu Ala Asp Thr Met Leu
 160

<210> 225
 <211> 227
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 225
 Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
 -20 -15 -10
 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
 -5 1 5 10
 Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
 15 20 25
 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
 30 35 40
 Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
 45 50 55
 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
 60 65 70
 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
 75 80 85 90
 Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
 95 100 105
 Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
 110 115 120
 Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
 125 130 135
 Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
 140 145 150
 Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
 155 160 165 170
 Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
 175 180 185
 Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
 190 195 200
 Ala Ala Cys
 205

<210> 226
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
<221> SIGNAL
<222> -41...-1

<400> 226
Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu
-40 -35 -30
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr
-25 -20 -15 -10
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg
-5 1 5
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile
10 15 20
Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu
25 30

<210> 227
<211> 73
<212> PRT
<213> Homo sapiens

<400> 227
Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly
1 5 10 15
Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile
20 25 30
Lys Lys Phe Leu Glu Ser Asp Asp Asp Lys Met Val Lys Lys Ile Ala
35 40 45
Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val
50 55 60
Asn Leu Leu Glu Val Cys Lys Lys Lys
65 70

<210> 228
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 228
Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser
-15 -10 -5
Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp
1 5 10 15
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr
20 25 30
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe
35 40 45
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg
50 55 60

Lys Asn
65

<210> 229
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -56...-1

<400> 229
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser
-55 -50 -45
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Ser Pro Gly
-40 -35 -30 -25
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp
-20 -15 -10
Ser Phe Val Ser Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr
-5 1 5
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu
10 15 20
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly
25 30 35 40
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro
45 50 55
Ile Leu Ala Lys Lys Lys Lys
60

<210> 230
<211> 54
<212> PRT
<213> Homo sapiens

<400> 230
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala
1 5 10 15
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys
20 25 30
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg
35 40 45
Gly Arg Gly Arg Pro His
50

<210> 231
<211> 210
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 231

Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val
-10 -5 1
Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr
5 10 15
Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu
20 25 30
Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile
35 40 45 50
Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe
55 60 65
Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met
70 75 80
Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu
85 90 95
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly
100 105 110
Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu
115 120 125 130
Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile
135 140 145
Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg
150 155 160
Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp
165 170 175
Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys
180 185 190
Gln Glu
195

<210> 232

<211> 108

<212> PRT

<213> Homo sapiens

<400> 232

Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1 5 10 15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20 25 30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
35 40 45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
50 55 60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65 70 75 80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
85 90 95
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
100 105

<210> 233
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 233
 Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu
 -15 -10 -5
 Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr
 1 5 10
 Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr
 15 20 25

<210> 234
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu
 5 10 15
 Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr
 20 25 30
 Phe Phe Gln Ile
 35

<210> 235
 <211> 307
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 235
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
 -10 -5 1
 Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
 5 10 15
 Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
 20 25 30 35
 Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
 40 45 50
 Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
 55 60 65
 Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
 70 75 80

Lys	Thr	Arg	Asp	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile	Arg
85						90					95				
Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Cys	Lys	Gly	Leu
100					105					110					115
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
			120						125					130	
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
			135					140					145		
Val	Ser	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser	Lys
		150					155					160			
Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp	Asp
		165				170					175				
Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val	Leu
180					185					190					195
Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala	Glu
			200						205					210	
Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile	Arg	Arg	Val
		215						220					225		
Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe	Val	Glu	Asn
		230					235					240			
Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser	Gly	Gly	Tyr
		245				250					255				
Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe	Ser	Met	Leu
260					265					270					275
Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile	Phe	Lys	Ala
				280					285					290	
Lys	Lys	Lys													

<210> 236
 <211> 106
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1

<400> 236
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
 1 5 10 15
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
 20 25 30
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
 35 40 45
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
 50 55 60
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
 65 70

<210> 237

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 237

Met	Asp	Leu	Arg	Gln	Phe	Leu	Met	Cys	Leu	Ser	Leu	Cys	Thr	Ala	Phe
				-15				-10						-5	
Ala	Leu	Ser	Lys	Pro	Thr	Glu	Lys	Lys	Asp	Arg	Val	His	His	Glu	Pro
			1			5					10				
Gln	Leu	Ser	Asp	Lys	Val	His	Asn	Asp	Ile						
	15				20										

<210> 238

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 238

Met	Asp	Asn	Arg	Phe	Ala	Thr	Ala	Phe	Val	Ile	Ala	Cys	Val	Leu	Ser
-20				-15				-10				-5			
Leu	Ile	Ser	Thr	Ile	Tyr	Met	Ala	Ala	Ser	Ile	Gly	Thr	Asp	Phe	Trp
			1			5					10				
Tyr	Glu	Tyr	Arg	Ser	Pro	Val	Gln	Glu	Asn	Ser	Ser	Asp	Leu	Asn	Lys
	15				20					25					
Ser	Ile	Trp	Asp	Glu	Phe	Ile	Ser	Asp	Glu	Ala	Asp	Glu	Lys	Thr	Tyr
	30				35				40						
Asn	Asp	Ala	Leu	Phe	Arg	Tyr	Asn	Gly	Thr	Val	Gly	Leu	Trp	Gly	Arg
45				50				55						60	
Cys	Ile	Thr	Ile	Pro	Lys	Asn	Met	His	Trp	Tyr	Ser	Pro	Pro	Glu	Arg
		65					70					75			
Thr	Gly	Ile	Ser	Leu	Ile	Leu	Thr	Ser	Val	Phe	Phe	Thr	Trp	Leu	Ile
		80					85						90		
Ile	Asp	Lys	Thr	Thr											
		95													

<210> 239

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 239

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Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
  -35                      -30                      -25
Gln His Xaa Xaa Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile
  -20                      -15                      -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
  -5                      1                      5                      10
Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu
      15                      20                      25
Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val
      30                      35                      40
Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn
      45                      50                      55
Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln
      60                      65                      70                      75
His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr
      80                      85                      90
Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe
      95                      100                      105
His Ala Gly Tyr Ser Leu Lys Lys Arg His Phe Phe Gln Asn Leu Gly
      110                      115                      120
Ser Ile Leu Thr Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Ile Val
      125                      130                      135
Ile Gly
140

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<210> 240

<211> 126

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 240

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Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val
  -25                      -20                      -15
Val Leu Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser
  -10                      -5                      1                      5
Met Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe Ile
      10                      15                      20
Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr Met Ala
      25                      30                      35
Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr
      40                      45                      50
Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met Lys Gly
      55                      60                      65
Leu Lys Cys Arg Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro
      70                      75                      80                      85
Tyr Phe Lys Met His Lys Pro Val Thr Met Lys Lys Lys Lys
      90                      95

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<210> 241
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -115..-1

<400> 241
Met Arg Trp Ser Cys Glu His Leu Val Met Val Trp Ile Asn Ala Phe
-115 -110 -105 -100
Val Met Leu Thr Thr Gln Leu Leu Pro Ser Lys Tyr Cys Asp Leu Leu
-95 -90 -85
His Lys Ser Ala Ala His Leu Gly Lys Trp Gln Lys Leu Glu His Gly
-80 -75 -70
Ser Tyr Ser Asn Ala Pro Gln His Ile Trp Ser Glu Asn Thr Ile Trp
-65 -60 -55
Pro Gln Gly Val Leu Val Arg His Ser Arg Cys Leu Tyr Arg Ala Met
-50 -45 -40
Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg Phe
-35 -30 -25 -20
Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile Leu
-15 -10 -5
Ile Glu Gly Gly Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg Ser
1 5 10
Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys Asn
15 20 25
Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Ile Val Leu Gly Arg
30 35 40 45
Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn
50 55

<210> 242
<211> 896
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..173

<221> sig_peptide
<222> 18..77
<223> Von Heijne matrix
score 6.5
seq GLCVLQLTTAVTS/AF

<221> polyA_signal
<222> 864..869

<221> polyA_site
<222> 882..893

<400> 242

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aaccttcaca gtgtgag atg cct agt gtg aac agt gct gga tta tgt gtc      50
                Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val
                -20                -15                -10
ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg      98
Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val
                -5                1                5
aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc      146
Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala
                10                15                20
cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcctgattca      193
His His Phe Ile His Pro Cys Leu Asp
                25                30
aagtgttacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgcttcag      253
agagggcagc acttatacct ggtgggtcttt ctgatgggtca gttttattcc cctcctgaat      313
ccgaagcagg atctgaagaa gctgaagaaa aacaggacag tgagaaacca cttttagaac      373
tatgagtact acttttggtt aatgtgaaaa accctcacag aaagtcacg aggcaaaaag      433
aggcaggcag tggagtctcc ctgtcgacag taaagttgaa atggtgacgt ccactgctgg      493
ctttattgaa cagctaataa agatttattt attgtaatac ctcacagacg ttgtaccata      553
tccatgcaca tttagttgcc tgcctgtggc tggtaaggta atgtcatgat tcatcctctc      613
ttcagtgaga ctgagcctga tgtgttaaca aataggtgaa gaaagtcttg tgctgtattc      673
ctaatacaaaa gacttaatat attgaagtaa cactttttta gtaagcaaga taccttttta      733
tttcaattca cagaatggaa tttttttgtt tcatgtctca gatttatttt gtatttcctt      793
tttaacactc tacatttccc ttgtttttta actcatgcac atgtgctctt tgtacagttt      853
taaaaaagtg aataaaatct gacatgtcaa aaaaaaaaaa mcy      896

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<210> 243

<211> 851

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 17..595

<221> sig_peptide

<222> 17..85

<223> Von Heijne matrix

score 3.70000004768372

seq FLPLPLXRAFACRG/CQ

<221> polyA_signal

<222> 820..825

<221> polyA_site

<222> 840..851

<400> 243

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aagggggcgt ggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc      52
                Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
                -20                -15
ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg      100
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
                -10                -5                1                5
gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga      148
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg

```


			10				15				20					
ttc	tgc	cct	cca	aga	aag	tct	tgc	cat	gat	tgg	ata	gga	ccc	cca	gat	196
Phe	Cys	Pro	Pro	Arg	Lys	Ser	Cys	His	Asp	Trp	Ile	Gly	Pro	Pro	Asp	
			25				30				35					
aaa	tat	tca	aac	ctt	cga	cct	gtt	cac	ttt	tac	ata	cct	gaa	aat	gaa	244
Lys	Tyr	Ser	Asn	Leu	Arg	Pro	Val	His	Phe	Tyr	Ile	Pro	Glu	Asn	Glu	
			40				45				50					
tct	cca	ttg	gaa	caa	aag	ctt	aga	aaa	tta	aga	caa	gaa	aca	caa	gaa	292
Ser	Pro	Leu	Glu	Gln	Lys	Leu	Arg	Lys	Leu	Arg	Gln	Glu	Thr	Gln	Glu	
			55				60				65					
tgg	aat	caa	cag	ttc	tgg	gca	aac	cag	aat	ttg	act	ttt	agt	aag	gaa	340
Trp	Asn	Gln	Gln	Phe	Trp	Ala	Asn	Gln	Asn	Leu	Thr	Phe	Ser	Lys	Glu	
			70				75				80				85	
aaa	gaa	gaa	ttt	att	cac	tca	aga	cta	aaa	act	aaa	ggc	ctg	ggc	ctg	388
Lys	Glu	Glu	Phe	Ile	His	Ser	Arg	Leu	Lys	Thr	Lys	Gly	Leu	Gly	Leu	
			90				95				100					
aga	act	gaa	tca	ggt	cag	aaa	gca	aca	ttg	aat	gca	gaa	gaa	atg	gcg	436
Arg	Thr	Glu	Ser	Gly	Gln	Lys	Ala	Thr	Leu	Asn	Ala	Glu	Glu	Met	Ala	
			105				110				115					
gac	ttc	tac	aag	gaa	ttt	tta	agt	aaa	aat	ttt	cag	aag	cac	atg	tat	484
Asp	Phe	Tyr	Lys	Glu	Phe	Leu	Ser	Lys	Asn	Phe	Gln	Lys	His	Met	Tyr	
			120				125				130					
tat	aac	aga	gat	tgg	tac	aag	cgc	aat	ttt	gcc	atc	acc	ttc	ttc	atg	532
Tyr	Asn	Arg	Asp	Trp	Tyr	Lys	Arg	Asn	Phe	Ala	Ile	Thr	Phe	Phe	Met	
			135				140				145					
gga	aaa	gtg	gcc	ctg	gaa	agg	att	tgg	aac	aag	ctt	aaa	cag	aaa	caa	580
Gly	Lys	Val	Ala	Leu	Glu	Arg	Ile	Trp	Asn	Lys	Leu	Lys	Gln	Lys	Gln	
			150				155				160				165	
aag	aag	agg	agc	aac	taggag	tcca	ctctgaccca	gccagag	tcc	aggtttccac						635
Lys	Lys	Arg	Ser	Asn												
			170													
aggaag	cara	tggag	ctcct	ttcac	agggg	ctctg	agaaa	aactg	gagct	gatct	caaga					695
agcccc	acat	cttccta	aagg	ggcccc	atgg	cctgt	tttggg	ggcagg	gtag	gtcct	ggggc					755
actgt	ggggc	gcctg	cctgc	tgatg	tgggc	tctagg	ccag	cttgt	gttca	cgtac	gtgg					815
gtgaa	ataaaa	gccaag	cac	tggg	aaaaaa	aaaaaa										851

<210> 244

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 89..334

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<221> sig peptide
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<222> 89..130

<223> Von Heijne matrix

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score 3.599999990463257
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seq AFTLXSLLQAALL/CV

<221> polyA signal

<222> 462..467

<221> polyA site

<222> 484..495

<400> 244

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agtaggaasg cgccgscctg ggagggcgcca cgtcccttgc sgcgggcgga gagamatcgc      60
ttggacttcg gggcggcctc ggacggcc atg gcc ttt acc ctg tas tca ctg      112
                               Met Ala Phe Thr Leu Xaa Ser Leu
                               -10
ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag      160
Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu
-5                               1                               5                               10
gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt      208
Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly
                               15                               20                               25
gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att      256
Gly Phe Gly Glu Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile
                               30                               35                               40
cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca      304
Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser
                               45                               50                               55
att gca att gtg tta ctt tta tta ttt gga tgaatwcat tggagaaaaat      354
Ile Ala Ile Val Leu Leu Leu Leu Phe Gly
60                               65
ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatattt      414
atatcttagc tggctgacct tgcacttgtc aaaaatgtaa agctgaaaat aaaaccaggg      474
tttctattta aaaaaaaaaa a      495

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<210> 245

<211> 884

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..614

<221> sig_peptide

<222> 21..83

<223> Von Heijne matrix

score 10

seq LWALAMVTRPASA/AP

<221> polyA_signal

<222> 849..854

<221> polyA_site

<222> 873..884

<400> 245

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aataccttag accctcagtc atg cca gtg cct gct ctg tgc ctg ctc tgg gcc      53
                               Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala
                               -20                               -15
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca      101
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro
-10                               -5                               1                               5
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg      149

```

Glu	Leu	Ala	Gln	His	Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu		
			10					15					20				
cag	ctg	ggc	cag	gcc	ctc	aac	ggg	gtg	tac	agg	acc	acg	gag	gga	cgg	197	
Gln	Leu	Gly	Gln	Ala	Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Arg		
		25					30					35					
ctg	aca	aag	gcc	agg	aac	agc	ctg	ggg	ctc	tat	ggc	cgc	aca	ata	gaa	245	
Leu	Thr	Lys	Ala	Arg	Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu		
	40					45					50						
ctc	ctg	ggg	cag	gag	gtc	agc	cgg	ggc	cgg	gat	gca	gcc	cag	gaa	ctt	293	
Leu	Leu	Gly	Gln	Glu	Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu	Leu		
55					60					65				70			
cgg	gca	agc	ctg	ttg	gaa	act	car	atg	gag	gag	gat	att	ctg	cas	ctg	341	
Arg	Ala	Ser	Leu	Leu	Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu	Xaa	Leu		
			75						80				85				
cag	gca	rag	gcc	aca	gct	gag	gtg	ctg	ggg	gag	gtg	gcc	cag	gca	car	389	
Gln	Ala	Xaa	Ala	Thr	Ala	Glu	Val	Leu	Gly	Glu	Val	Ala	Gln	Ala	Gln		
			90					95				100					
aag	gtg	cta	cgg	gac	agc	gtg	cag	cgg	cta	daa	ktc	cag	ctg	arg	asc	437	
Lys	Val	Leu	Arg	Asp	Ser	Val	Gln	Arg	Leu	Xaa	Xaa	Gln	Leu	Xaa	Xaa		
		105					110					115					
gcc	tgg	ctg	ggc	cct	gcc	tac	cga	aaa	ttt	gar	gtc	tta	aag	gcy	ccc	485	
Ala	Trp	Leu	Gly	Pro	Ala	Tyr	Arg	Lys	Phe	Glu	Val	Leu	Lys	Ala	Pro		
		120				125					130						
cck	gam	aar	car	aac	cac	atc	cta	tgg	gcc	ctc	aca	ggc	cac	gtg	cak	533	
Pro	Xaa	Lys	Gln	Asn	His	Ile	Leu	Trp	Ala	Leu	Thr	Gly	His	Val	Xaa		
		135				140				145				150			
cgg	car	arg	cgg	gar	atg	gtg	gca	cag	cag	cwt	ckg	ctg	cna	car	atc	581	
Arg	Gln	Xaa	Arg	Glu	Met	Val	Ala	Gln	Gln	Xaa	Xaa	Leu	Xaa	Gln	Ile		
				155				160				165					
cag	gar	aaa	ctc	cac	aca	gcy	gcy	ctc	cca	gcc	tgaatctgcc	tgatggaac				634	
Gln	Glu	Lys	Leu	His	Thr	Ala	Ala	Leu	Pro	Ala							
			170					175									
tgaggacca	aa	tc	atgctgca	aggaacactt	ccacgccccg	tgaggccccct	gtgcagggag									694	
gagctgcctg	ttcactggga	tcagccaggg	cgccggggccc	cacttctgag	cacagagcar											754	
agacagacgc	aggcggggac	aaaggcagag	gatgtagccc	cattggggag	gggtggagga											814	
aggacatgta	ccctttcatr	mctacacacc	cctcattaaa	gcavagtcgt	ggcatctcaa											874	
aaaaaaaaaa																884	

<210> 246
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..573

<221> sig_peptide
 <222> 94..258
 <223> Von Heijne matrix
 score 4.69999980926514
 seq IGILCSLLGTVLL/WV

<221> polyA_signal
 <222> 862..867

<221> polyA_site

<222> 886..897

<400> 246

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aagggcggct gcctagcacc cggaagagcc gtcaacttag cgagcgcaac aggctgccgc      60
tgaggagctg gagctggtgg ggactgggcc gca atg gac aag ctg aag aag gtg      114
                               Met Asp Lys Leu Lys Lys Val
                               -55                               -50

ctg agc ggg cag gac acg gag gac cgg agc ggc ctg tcc gag gtt gtt      162
Leu Ser Gly Gln Asp Thr Glu Asp Arg Ser Gly Leu Ser Glu Val Val
                               -45                               -40                               -35

gag gca tct tca tta agc tgg agt acc agg ata aaa ggc ttc att gcg      210
Glu Ala Ser Ser Leu Ser Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala
                               -30                               -25                               -20

tgt ttt gct ata gga att ctc tgc tca ctg ctg ggt act gtt ctg ctg      258
Cys Phe Ala Ile Gly Ile Leu Cys Ser Leu Leu Gly Thr Val Leu Leu
                               -15                               -10                               -5

tgg gtg ccc agg aag gga cta cac ctc ttc gca gtg ttt tat acc ttt      306
Trp Val Pro Arg Lys Gly Leu His Leu Phe Ala Val Phe Tyr Thr Phe
1                               5                               10                               15

ggg aat atc gca tca att ggg agt acc atc ttc ctc atg gga cca gtg      354
Gly Asn Ile Ala Ser Ile Gly Ser Thr Ile Phe Leu Met Gly Pro Val
                               20                               25                               30

aaa cag ctg aag cga atg ttt gag cct act cgt ttg att gca act atc      402
Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile
                               35                               40                               45

atg gtg ctg ttg tgt ttt gca ctt acc ctg tgt tct gcc ttt tgg tgg      450
Met Val Leu Leu Cys Phe Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp
50                               55                               60

cat aac aag gga ctt gca ctt atc ttc tgc att ttg cag tct ttg gca      498
His Asn Lys Gly Leu Ala Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala
65                               70                               75                               80

ttg acg tgg tac agc ctt tcc ttc ata cca ttt gca agg gat gct gtg      546
Leu Thr Trp Tyr Ser Leu Ser Phe Ile Pro Phe Ala Arg Asp Ala Val
85                               90                               95

aaa aad tgt ttt gcc gtg tgt ctt gca taattcatgg ccagttttat      593
Lys Xaa Cys Phe Ala Val Cys Leu Ala
100                               105

gaagctttgg aaggcactat ggacagaagc tgggtggacag ttttgtwact atcttcgaaa      653
cctctgtctt acagacatgt gcctttttatc ttgcagcaat gtgttgcttg tgattcgaac      713
atttgagggg tactttttgga agcaacaata cattctcgaa cctgaatgtc agtagcacag      773
gatgagaagt gggttctgta tcttgtggag tggaatcttc ctcatgtacc tgtttcctct      833
ctggatgttg tcccactgaa ttcccatgaa tacaaaccta ttcagcaaca gcaaaaaaaaa      893
aaaa                                                                897
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<210> 247

<211> 518

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 74..397

<221> sig_peptide
 <222> 74..127
 <223> Von Heijne matrix
 score 7.69999980926514
 seq LLLLPVLGLLVSS/KT

<221> polyA_signal
 <222> 472..477

<221> polyA_site
 <222> 507..518

<400> 247
 aaagaaagag ctgcsgtgca ggaattcgtg tgccggattt ggtagctga gcccaccgag 60
 aggcgcctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg 109
 Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu
 -15 -10
 ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc 157
 Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
 -5 1 5 10
 aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata 205
 Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
 15 20 25
 agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg 253
 Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
 30 35 40
 gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc 301
 Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
 45 50 55
 gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag 349
 Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
 60 65 70
 tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc 397
 Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
 75 80 85 90
 tgaggtcgcg cgcagcgcg gcacagcgcg ggcggaggcg gctccaggct cggaggggtt 457
 gcgggggagc tggaaataaa cctggagatg atgatgatga tgatgatgga aaaaaaaaaa 517
 518

<210> 248
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 51..242

<221> sig_peptide
 <222> 51..116
 <223> Von Heijne matrix
 score 6.5
 seq SCLCPALFPGTSS/FI

<221> polyA_signal

<222> 319..324

<221> polyA_site

<222> 339..350

<400> 248

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acgtcattcc aaaaccacac ccttgcaaag ctttgtactc cgcaccccag atg atc      56
                                     Met Ile
tcc agg cag ctc aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc      104
Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro
-20          -15          -10          -5
ggg act tcc tcc ttt att gta gca ctc agc tcc cca gcc gat ctg tac      152
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr
          1          5          10
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa      200
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys
          15          20          25
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta      242
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val
          30          35          40
tgatttttgct gaatttttaaa taaaatgaaa accataaatt acatratgct tttattgach      302
cttgacmact ggcctaaata aaaaaractct gactccaaaa aaaaaaaaa      350
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<210> 249

<211> 996

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 111..191

<221> sig_peptide

<222> 111..155

<223> Von Heijne matrix
score 5.80000019073486
seq FLXLMTLTTHVHS/SA

<221> polyA_signal

<222> 965..970

<221> polyA_site

<222> 986..996

<400> 249

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atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggtga tttccgagct      60
cagcaatgct cagctcataa tgatgtcaag caccatggcc agttttatga atg ggy      116
                                     Met Gly
                                     -15
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag      164
Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser Ala Lys
          -10          -5          1
cca aat gaa caa ccc tgg ttg ttg aac tagcacctaa ggtcttarat      211
Pro Asn Glu Gln Pro Trp Leu Leu Asn
          5          10
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ggtacgcgtt gctatacaga atctttggat atgtgcatca gtgggtttatg ccaaattggt 271
ggctgcgatc accagctggg aagcaccgtc aaggaarata actgtggggg ctgcaacrga 331
natgggtcca cctgccggct ggtccgaggg cartataaat cccakctctc cgcaacccaaa 391
tcr gatgata ctgtgggttgc aattccctat ggaagtakac atattcgctt tgtcttaaaa 451
ggtcctgatc acttataatc ggaarccawa accctccagg ggactaawgg tgaaaacagt 511
ctcasctcca caggaacttt ccttgtggac aattctagt tggacttcca gaawtttcca 571
gacwdagaga tactgagaat ggctggacca ctcacagcag atttcattgt caawattcgt 631
aactcgggct ccgctgacag tacagtccag kkcattcttct atcaacccat catccaccga 691
tggagggara cggattttctt tccttgctca gcaacctgtg gaggagggtta tcagctgaca 751
tcggctgagt gctacgatct gaggagcaac cgtgtgggtg ctgaccaata ctgtcactat 811
taccagaga acatcaaacc caaacccaag cttcaggagt gcaacttgga tccttgtcca 871
gccaggtcag tcaaatattgc tagttcattt gtcataaaca taactcaagt tccaaatagg 931
ttatttaaat taaaatgaaa cgttttaatt aaaaataaaa tgaaattaaa catcaaaaaa 996
aaaaa

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<210> 250

<211> 860

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 45..602

<221> sig_peptide

<222> 45..107

<223> Von Heijne matrix

score 8.5

seq LLTIVGLILPTRG/QT

<221> polyA_signal

<222> 828..833

<221> polyA_site

<222> 850..860

<400> 250

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acctctctcc acgaggetgc cggettagga cccccagctc cgac atg tcg ccc tct 56
Met Ser Pro Ser

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-20

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ggt cgc ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga 104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg

```

-15

-10

-5

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gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act 152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr

```

1

5

10

15

```

atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca 200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr

```

20

25

30

```

gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca 248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr

```

35

40

45

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cca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct 296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro

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50

55

60

cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc	344
Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro	
65 70 75	
act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac	392
Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa	
80 85 90 95	
gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt ttc atg agg	440
Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg	
100 105 110	
atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt	488
Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys	
115 120 125	
tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg	536
Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Ser Pro Val	
130 135 140	
gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag	584
Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu	
145 150 155	
tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag	632
Ser Ile Arg Asn Arg Ser	
160 165	
ccccctgccg gctcaccgtg cccagcctcc tgcacccccct cgaagagcct ggccagagag	692
ggaagacaca gatgatgaag ctggagccag ggctgcccgt cagagtctcc tacctcccc	752
aacctgccc gcccctgaag gctacctggc gccttggggg ctgtccctca agttatctcc	812
tctgctaaga caaaaagtaa agcactgtgg tctttgcaaa aaaaaaaaa	860

<210> 251

<211> 593

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 24..560

<221> sig_peptide

<222> 24..101

<223> Von Heijne matrix

score 10.3999996185303

seq LLLLLCGPSQDQC/RP

<221> polyA_signal

<222> 563..568

<221> polyA_site

<222> 583..593

<400> 251

aanccagctg csgccggcca gcc atg gag act gga gcg ctg cgg cgc ccg caa	53
Met Glu Thr Gly Ala Leu Arg Arg Pro Gln	
-25 -20	

ctt ctc ccg ttg ctg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc	101
Leu Leu Pro Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys	
-15 -10 -5	

cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc	149
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Arg	Pro	Val	Leu	Gln	Asn	Leu	Leu	Gln	Ser	Pro	Gly	Leu	Thr	Trp	Ser	
1				5					10					15		
ttg	gaa	gtg	ccc	act	ggg	aga	gaa	gga	aag	gaa	ggg	gat	cgg	gga		197
Leu	Glu	Val	Pro	Thr	Gly	Arg	Glu	Gly	Lys	Glu	Gly	Gly	Asp	Arg	Gly	
			20					25					30			
cca	ggg	cta	akt	ggg	gcc	act	cca	gcc	agg	agc	cct	cag	ggc	aag	gag	245
Pro	Gly	Leu	Xaa	Gly	Ala	Thr	Pro	Ala	Arg	Ser	Pro	Gln	Gly	Lys	Glu	
		35					40					45				
atg	ggg	aga	caa	agg	acc	aga	aag	gtg	aag	ggc	cct	gct	tgg	akt	cac	293
Met	Gly	Arg	Gln	Arg	Thr	Arg	Lys	Val	Lys	Gly	Pro	Ala	Trp	Xaa	His	
	50					55					60					
aca	gca	aat	cag	gaa	cta	aac	agg	atg	agg	tct	ctg	tct	tct	ggc	tcc	341
Thr	Ala	Asn	Gln	Glu	Leu	Asn	Arg	Met	Arg	Ser	Leu	Ser	Ser	Gly	Ser	
65					70				75					80		
gtg	cca	gtg	ggg	cat	ctg	gag	ggg	ggc	acg	gtc	aag	ctt	cag	aag	gac	389
Val	Pro	Val	Gly	His	Leu	Glu	Gly	Gly	Thr	Val	Lys	Leu	Gln	Lys	Asp	
			85						90				95			
acg	ggc	ctc	cat	tcc	tgc	ara	gat	ggg	atg	gct	tct	ctt	gaa	ggg	acg	437
Thr	Gly	Leu	His	Ser	Cys	Xaa	Asp	Gly	Met	Ala	Ser	Leu	Glu	Gly	Thr	
		100						105				110				
cca	gct	tca	gtc	ctg	gct	gat	gct	tgc	cca	gga	ttc	cat	gat	gtg	aan	485
Pro	Ala	Ser	Val	Leu	Ala	Asp	Ala	Cys	Pro	Gly	Phe	His	Asp	Val	Xaa	
		115					120					125				
gtt	car	arg	gcc	cta	ttt	ggg	tta	agt	ggg	ana	rta	ctg	tgg	ctg	aaa	533
Val	Gln	Xaa	Ala	Leu	Phe	Gly	Leu	Ser	Gly	Xaa	Xaa	Leu	Trp	Leu	Lys	
		130				135					140					
acc	cac	ttc	tgc	ctt	tct	att	ana	ctt	taaataaaact	ctgaaracct						580
Thr	His	Phe	Cys	Leu	Ser	Ile	Xaa	Leu								
145					150											
gt	aaaaaaaaa	aaa														593

<210> 252
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 109..558

<221> sig_peptide
 <222> 109..273
 <223> Von Heijne matrix
 score 3.70000004768372
 seq VAFMLTLPILVCK/VQ

<221> polyA_site
 <222> 1104..1114

<400> 252
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 ggaagcagca ccaagttcac ggccaacgcc ttggcactag ggtccaga atg gct aca 117
 Met Ala Thr
 -55
 aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga 165

Thr	Val	Pro	Asp	Gly	Cys	Arg	Asn	Gly	Leu	Lys	Ser	Lys	Tyr	Tyr	Arg		
	-50						-45					-40					
ctt	tgt	gat	aag	gct	gaa	gct	tgg	ggc	atc	gtc	cta	gaa	acg	gtg	gcc	213	
Leu	Cys	Asp	Lys	Ala	Glu	Ala	Trp	Gly	Ile	Val	Leu	Glu	Thr	Val	Ala		
	-35						-30					-25					
aca	gcc	ggg	gtt	gtg	acc	tcg	gtg	gcc	ttc	atg	ctg	act	ctc	ccg	atc	261	
Thr	Ala	Gly	Val	Val	Thr	Ser	Val	Ala	Phe	Met	Leu	Thr	Leu	Pro	Ile		
	-20					-15				-10					-5		
ctc	gtc	tgc	aag	gtg	cag	gac	tcc	aac	agg	cga	aaa	atg	ctg	cct	act	309	
Leu	Val	Cys	Lys	Val	Gln	Asp	Ser	Asn	Arg	Arg	Lys	Met	Leu	Pro	Thr		
			1					5				10					
cag	ttt	ctc	ttc	ctc	ctg	ggt	gtg	ttg	ggc	atc	ttt	ggc	ctc	acc	ttc	357	
Gln	Phe	Leu	Phe	Leu	Leu	Gly	Val	Leu	Gly	Ile	Phe	Gly	Leu	Thr	Phe		
	15						20					25					
gcc	ttc	atc	atc	gga	ctg	gac	ggg	agc	aca	ggg	ccc	aca	cgc	ttc	ttc	405	
Ala	Phe	Ile	Ile	Gly	Leu	Asp	Gly	Ser	Thr	Gly	Pro	Thr	Arg	Phe	Phe		
	30					35					40						
ctc	ttt	ggg	atc	ctc	ttt	tcc	atc	tgc	ttc	tcc	tgc	ctg	ctg	gct	cat	453	
Leu	Phe	Gly	Ile	Leu	Phe	Ser	Ile	Cys	Phe	Ser	Cys	Leu	Leu	Ala	His		
	45				50				55					60			
gct	gtc	agt	ctg	acc	aag	ctc	gtc	cgg	ggg	agg	aaa	gcc	cct	ttc	cct	501	
Ala	Val	Ser	Leu	Thr	Lys	Leu	Val	Arg	Gly	Arg	Lys	Ala	Pro	Phe	Pro		
			65					70				75					
gtt	ggt	gat	tct	ggg	tct	ggc	cgt	ggg	ctt	cag	cct	agt	cca	gga	tgt	549	
Val	Gly	Asp	Ser	Gly	Ser	Gly	Arg	Gly	Leu	Gln	Pro	Ser	Pro	Gly	Cys		
			80					85				90					
tat	cgc	tat	tgaatatatt	gtcctgacca	tgaataggac	caacgtcaat										598	
Tyr	Arg	Tyr															
	95																
gtctttttctg	agctttccgc	tcctcgtcgc	aatgaaaact	ttgtcctcct	gctcacctac											658	
ktcctcttct	tgatggcgct	gaccttcctc	wtgtcctcct	tcaccttctg	tggtkccttc											718	
acgggctgga	avagacatgg	ggccacatc	tacctcasga	tgetcskctc	cattgccatc											778	
tggttgccct	ggatcaccct	gctcatgctt	cctgactttg	accgcragg	ggatgacacc											838	
atcmtcarct	ccgccttggs	trcsaatggc	tgggtgttcc	tggttgctta	tgtagtccc											898	
gagttttggc	tgctcacaaa	gcaackaaac	cccatggatt	atcctgttga	ggatgctttc											958	
tgtaaacctc	aactcgtgaa	gaagagctat	ggtgtggrga	acagagccta	skctcaagag											1018	
gaaatcactc	aagggtttga	agagacaggg	gacacgctct	atgcccccta	ttccacacat											1078	
tttcagctgc	agaascagcc	tccccaaaaa	aaaaaa													1114	

<210> 253

<211> 1182

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..835

<221> sig_peptide

<222> 128..220

<223> Von Heijne matrix

score 4.69999980926514

seq LAVDSWWLDPGHA/AV

<221> polyA_signal

<222> 1145..1150

<221> polyA_site

<222> 1170..1181

<400> 253

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ccgccg	ccgt	ttcctg	attg	gttgtg	gggtg	gctac	ctctt	cg	ttctg	att	ggccg	ctagt		120
gagcaag	atg	ctg	agc	aag	ggt	ctg	aag	cgg	aaa	cgg	gag	gag	gag	169
	Met	Leu	Ser	Lys	Gly	Leu	Lys	Arg	Lys	Arg	Glu	Glu	Glu	
		-30					-25				-20			
gag	aag	gaa	cct	ctg	gca	gtc	gac	tcc	tgg	tgg	cta	gat	cct	217
Glu	Lys	Glu	Pro	Leu	Ala	Val	Asp	Ser	Trp	Trp	Leu	Asp	Pro	
		-15					-10				-5			
gca	gcg	gtg	gca	cag	gca	ccc	ccg	gcc	gtg	gcc	tct	agc	tcc	265
Ala	Ala	Val	Ala	Gln	Ala	Pro	Pro	Ala	Val	Ala	Ser	Ser	Ser	
	1			5					10				15	
gac	ctc	tca	gtg	ctc	aag	ctc	cac	cac	agc	ctg	cag	vrr	agt	313
Asp	Leu	Ser	Val	Leu	Lys	Leu	His	His	Ser	Leu	Gln	Xaa	Ser	
			20					25				30		
gac	ctg	cgg	cac	ctg	gtg	ctg	gtc	atr	aac	act	ctg	cgg	cgc	361
Asp	Leu	Arg	His	Leu	Val	Leu	Val	Xaa	Asn	Thr	Leu	Arg	Arg	
			35					40				45		
gcg	tcc	atg	gca	ccc	gcg	gct	gcc	ctg	cca	cct	gtg	cct	acc	409
Ala	Ser	Met	Ala	Pro	Ala	Ala	Ala	Leu	Pro	Pro	Val	Pro	Thr	
		50					55				60			
gca	gcc	ccc	ant	gtg	gct	gac	aac	tta	ctg	gca	agc	tcg	gac	457
Ala	Ala	Pro	Xaa	Val	Ala	Asp	Asn	Leu	Leu	Ala	Ser	Ser	Asp	
		65				70				75				
ctt	tca	gcc	tcc	atg	gcc	arm	ctc	ctg	gar	gac	ctc	agc	cac	505
Leu	Ser	Ala	Ser	Met	Ala	Xaa	Leu	Leu	Glu	Asp	Leu	Ser	His	
		80			85				90				95	
ggc	ctg	agt	cag	gct	ccc	caa	ccc	ttg	gca	gac	gag	ggg	cca	553
Gly	Leu	Ser	Gln	Ala	Pro	Gln	Pro	Leu	Ala	Asp	Glu	Gly	Pro	
			100					105					110	
cg	agc	atc	ggg	gga	wca	ccg	ccc	amc	ctg	gg	gcc	ttg	gac	601
Arg	Ser	Ile	Gly	Gly	Xaa	Pro	Pro	Xaa	Leu	Gly	Ala	Leu	Asp	
			115					120					125	
ggc	cca	gcc	act	ggc	tgt	cta	ctg	gac	aat	ggg	ctt	gag	ggc	649
Gly	Pro	Ala	Thr	Gly	Cys	Leu	Leu	Asp	Asn	Gly	Leu	Glu	Gly	
		130					135					140		
gag	gat	att	gac	acc	tct	atg	tat	gac	aat	gaa	ctt	tgg	gca	697
Glu	Asp	Ile	Asp	Thr	Ser	Met	Tyr	Asp	Asn	Glu	Leu	Trp	Ala	
		145				150				155				
tct	gag	ggc	ctc	aaa	cca	ggc	cct	gag	gat	ggg	ccg	ggc	aag	745
Ser	Glu	Gly	Leu	Lys	Pro	Gly	Pro	Glu	Asp	Gly	Pro	Gly	Lys	
		160			165				170				175	
gct	ccg	gag	ctg	gac	gag	gcc	gaa	ttg	gac	tac	ctc	atg	gat	793
Ala	Pro	Glu	Leu	Asp	Glu	Ala	Glu	Leu	Asp	Tyr	Leu	Met	Asp	
			180					185				190		
gtg	ggc	aca	cag	gca	ctg	gag	cga	ccg	ccg	ggg	cca	ggg	cgc	835
Val	Gly	Thr	Gln	Ala	Leu	Glu	Arg	Pro	Pro	Gly	Pro	Gly	Arg	
			195					200				205		
tgagcc	ctcg	tgctg	gaatg	gttgt	ctggt	atctga	actg	agcct	gctg	ctgg	acca	ac		895
tg	ctctg	aa	aagac	acagc	tg	gctt	ccct	ag	tacag	aga	acagg	gctt	g	955
gag	acaga	at	ctag	tcc	ggg	caact	tc	acat	ccg	tcc	tcct	gtct	ca	1015
ggg	gag	cctg	gaatt	acccc	ctag	t	gatg	aat	gac	agg	tct	ggtg	ggg	1075

ctggccctgg ggtcatagct tgggctgttc cttctctgat acggaagag acccaatcag 1135
atttttcaaa ttaaagccag tcttgggaaa tctcaaaaaa aaaaaaac 1182

<210> 254
<211> 1073
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..505

<221> sig_peptide
<222> 59..358
<223> Von Heijne matrix
score 3.70000004768372
seq LASSFLFTMGGLG/FI

<221> polyA_signal
<222> 1042..1047
<221> polyA_site
<222> 1062..1073

<400> 254
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atg gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac 106
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100 -95 -90 -85
ctg aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act 154
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
-80 -75 -70
gtg tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata 202
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
-65 -60 -55
att tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat 250
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
-50 -45 -40
gaa cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat 298
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
-35 -30 -25
gga caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg 346
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20 -15 -10 -5
gga ggt tta ggt ttc ata atc ctg gac gga tcg aat gca cca aat atc 394
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
1 5 10
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc 442
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
15 20 25
cta twr agt ttt ttc ayg gct aga gta ttc atg aga atg aaa ctg ccg 490
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
30 35 40
ggc tat ctg atg ggt tagagtgcct ttgasaagaa atcagtggat actggatttg 545
Gly Tyr Leu Met Gly

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45
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaatg tggaaaagaa 605
tgaagagcag cagtaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgga 665
ctagaatttc ttcttggtat taaagagaca agtttatcac agaatttttt ttctgtctgg 725
cctattgcta taccaatgat gttgagtggc attttctttt tagtttttca ttaaaatata 785
ttccatatct acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat 845
tttttgagga tgacatttct gatttttcaga aattaacata aaatccagaa gcaagattcc 905
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc ctttaactag 965
agtgtgtgat ggtagattat ttcagatatg tatgtaaaac tgtttcctga acaataagat 1025
gtatgaacgg agcagaaata aatacttttt ctaattaaaa aaaaaaaaa 1073

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<210> 255
<211> 818
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 1..207

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<221> sig_peptide
<222> 1..147
<223> Von Heijne matrix
      score 7.59999990463257
      seq HLPFLLLLSCVGX/XP

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<221> polyA_signal
<222> 784..789

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<221> polyA_site
<222> 807..818

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<400> 255
atg cct ttc cat ttt ccg ttc ctt ggg ttt gtg tgt ctg cat ctc cat 48
Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
      -45      -40      -35
ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg 96
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
      -30      -25      -20
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg 144
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
      -15      -10      -5
gkc www ccc tcc tgt ctg cct tct tcc tcc act tgt gtc agc ttg cat 192
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
      1      5      10      15
ttt ttt att cct gac tgagtcacca caccctctc ccctgatcaa aggggaatat 247
Phe Phe Ile Pro Asp
      20
artttttaat ttggatcgac tgaggtgccca ggagaaactg cagkcccagg tatccmvaca 307
gccaccagga tggtcctctg ccccccaccc accgcctctk cccacacctt tccaacgtgt 367
tgcatgctgg gaactggggg gtgtggggga aggggctgcc ggcttctttc aggangctga 427
rgtttggar caaaatcaac ctgggaracc accccggccg cggcgccctca gtggacaggt 487
gggargaaaa gaaaacttct taccttggar gargacatc ccgcttcctt atccttagct 547
ttttgttgct tcctcccac tgcccctttt aatttatatt gttgtttgct gaaggagggg 607
ggaagggggg aagctgggcc gggaactgtc cgaggtgctg agctggggcg ggaccggaat 667

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cctccccgta ggggtaccagg gactgagttg ggcctggggc cgtgtccaag gtgccaatga	727
tgccgggccga cagarcgggc cgcaactgtct gtctgtccgt ctgtcccga aagaactata	787
aagcgctgga agcgctgca aaaaaaaaaa a	818

<210> 256
<211> 971
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..734

<221> sig_peptide
<222> 12..101
<223> Von Heijne matrix
score 4.80000019073486
seq ILFCVGAVGACTL/SV

<221> polyA_signal
<222> 914..919

<221> polyA_site
<222> 961..971

<400> 256	
ataacacaga a atg ggg act gcg agc aga agc aac atc gct cgc cat ctg	50
Met Gly Thr Ala Ser Arg Ser Asn Ile Ala Arg His Leu	
-30 -25 -20	
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act	98
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr	
-15 -10 -5	
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag	146
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu	
1 5 10 15	
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag	194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu	
20 25 30	
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac	242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn	
35 40 45	
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg	290
Leu Cys Leu Asp Gly Cys Lys Ser Glu Ala Xaa Lys Phe Thr Val Arg	
50 55 60	
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act	338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr	
65 70 75	
tca aat gac agt gca att tac atc tgt gga ata gca ttc ccc agt gtg	386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val	
80 85 90 95	
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta	434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Thr Thr Leu Val Val	
100 105 110	
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct	482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala	

115	120	125	
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc			530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe			
130	135	140	
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata			578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile			
145	150	155	
aaa gaa gac tca caa aag aag aag agt gct cgg cgt att ttt cag gaa			626
Lys Glu Asp Ser Gln Lys Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu			
160	165	170	175
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa			674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln			
180	185	190	
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac			722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn			
195	200	205	
tat gaa agg cca tagaaacggt ttaattttca atgaagtcac tgaaaatcca			774
Tyr Glu Arg Pro			
210			
actccaggag ctatggcagt gttaatgaac atatatcatc aggtcttaaa aaaaaataaa			834
ggtaaaactga aaagacaact ggctacaaag aaggatgccca raatgtaagg aaactataac			894
taataktcat taccaaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa			954
tttgccaaaa aaaaaaw			971

<210> 257

<211> 640

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 378..518

<221> sig_peptide

<222> 378..467

<223> Von Heijne matrix

score 5.5

seq SLMTCTTLINASA/IS

<221> polyA_signal

<222> 607..612

<221> polyA_site

<222> 628..640

<400> 257

agcctgggta akgcccaaga tggctgtctt cgccttagta ctcgtgtgaa gttggcgggg	60
acggttcctg tcatcttctt gggcttattht ggtgtgctgt tgaagggggg agactagaga	120
aatggcaggg aacctcttat cgggggcagg taggcgcctg tgggactggg tgcctctggc	180
gtgcagaagc ttctctcttg gtgtgcctag attgatcggg ataaggctca ctctcccgcc	240
ccccaaagtg gttgatcgtt ggaacgagaa aagggccatg ttcggagtgt atgacaacat	300
cgggatcctg ggaaactttg aaaagcaccc caaagaactg atcagggggc ccatatggct	360
tcgaggttg aaagggga atg aat tgc aac gtt gta tcc gaa aga gga aaa	410
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys	

tgg ttg gaa gta gaa tgt tcg ctg atg acc tgc aca acc tta ata aac	458
Trp Leu Glu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn	
-15 -10 -5	
gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat	506
Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp	
1 5 10	
aga aga gaa agc tgagaacttc ggaaaaggct catctgtcac cctggaraag	558
Arg Arg Glu Ser	
15	
ggaaactgta cttttccctg tgaggaaacg gctttgtatt ttctctgtaa taaaatgggg	618
cttctttgga aaaaaaaaaa aa	640

<210> 258

<211> 745

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 110..304

<221> sig_peptide

<222> 110..193

<223> Von Heijne matrix

score 4.59999990463257

seq PLQWSLLVAVVAG/SV

<221> polyA_signal

<222> 708..713

<221> polyA_site

<222> 732..743

<400> 258

acttccgcct ggcctgctg agcvcagctc cshgagccct gccaacatg gtgaacttgg	60
gtctgtcccg ggtggacgac gccgtggctg ccaagcaccg ggcaccggc atg gcc ttt	118
Met Ala Phe	
ggc ttg cag atg ttc att cag agg aag ttt cca tac cct ttg cag tgg	166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp	
-25 -20 -15 -10	
agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg	214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val	
-5 1 5	
acg aga gtg gag tcg gag aaa tgc aac aac ctc tgg ctc ttc ctg gag	262
Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu	
10 15 20	
acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc	304
Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser	
25 30 35	
taggagagct ccagcagggg cacagargat tgggggcagg argartctgg aacacakcct	364
tcatgcccc tgaccccgagg ccgaccctcc ccacacccta gggtagccca gtcgtatcct	424
ctgtccgcat gtgtggccag gcctgacaaa cmcctgcaga tggctgctgc cccaacctgg	484
gacctgcccc ggaggttggg gcagaaaaggg ctctccctgg ggtggtgttt ctctctagg	544
gtattgggat gcatgttctg cactgccagc agagaggggtg tgtctggggg ccaccaccta	604
tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt cctttctagc ccctgcatct	664

ccaacaagtc caaggtgaca gctggtgcta ggggcgtggg gttaataaat ggcttatcct 724
tctctccaaa araaaaaaaaam c 745

<210> 259
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 201..419

<221> sig_peptide
<222> 201..272
<223> Von Heijne matrix
score 6.40000009536743
seq LSYLPLWLGPWP/CS

<221> polyA_signal
<222> 601..606

<221> polyA_site
<222> 627..637

<400> 259
acaaaatata attgcctcts ccctctccca ttttctctct tgggagcaat ggtcacagtc 60
cctggtacct gaaaagggtac ctaggtctag gcccttcttc cctttccctt cctctcccct 120
accccagaac tttggctccc tttcccttct ctctctggta gctccaggag gcctgtgatc 180
cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc 233
Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe
-20 -15
ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc 281
Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly
-10 -5 1
ctct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg 329
Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg
5 10 15
ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar 377
Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa
20 25 30 35
aac cak tat gav aak tgg ggg cag ggc aca cat tca tct ttg 419
Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu
40 45
targaaggtc tggcctgggg tcrpgtgaag gagggcccag gtcagttctg ggggtcccagt 479
gacctgcttt gccattctcc tgggtgccgct gctgctccct gtttctggag ctggatgttc 539
cccacctggc agttgagctg cctgagccaa tgtgtctgtc tttggttaact gagtgaacca 599
taataaaggg gaacatttgg ccctgtgaaa aaaaaaaaa 637

<210> 260
<211> 1315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 123..302

<221> sig_peptide
<222> 123..176
<223> Von Heijne matrix
score 4.30000019073486
seq WTCLKSFPSPTSS/HA

<221> polyA_signal
<222> 1279..1284

<221> polyA_site
<222> 1301..1312

<400> 260
aagagcatcc tgcgcccccg cgcgggggccc tgcggtagcc tcaggcccct cccctggacc 60
cgccgcagag ccagtgcaga atacagaaac tgcagccatg accacgcacg tcaccctgga 120
ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg 167
Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro
-15 -10 -5
acc agc agc cat gca tgc agc ctc cac ctt cct cca tca tgt acc agg 215
Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg
1 5 10
cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca 263
Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala
15 20 25
ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat 312
Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala
30 35 40
gctggaggaa ggacatgakt atgcggtcat gctgtacacc tggcgcagct gttccccgggc 372
cattccccag gtgaaatgca acragcagcc caaccgakta raratctatg araaracagt 432
aragggtgctg gagccggagg tcaccaagct catgaagttc atgtattttc arcgcaaggc 492
catcgagcgg ttctgcascg aggtgaagcg gctgtgccat gccgagcgca ggaaggactt 552
tgtctctgag gcctacctcc tgacccttgg caagtccatc aacatgtttg ctgtcctgga 612
tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc 672
acagttcctg cggaagatgg cagatcccca gtctatccag gagtcgcaga acctttccat 732
gttcctggcc aaccacaaca ggatcaccca gtgtctccac cagcaacttg aagtgatccc 792
aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa 852
gatgtacctg actcccagtg agaaacatat gtcctcaag gtaaaactcc cctgaggccg 912
caccatgga gcctgggctt accctctcac cttcttctta ttaaaaatcc gttttaaaaa 972
acaatgtttc ttttttctta aacattgata cagatcttac ggcacataat ggtttgtaac 1032
ctgttccttt cctgtaatat aatataccgt agtcaccttt ccagatgtca ttaaggctat 1092
ttctacaatg ttatgtgtaa tgactgcaa gtattctgtt gtattggaac attgtcatgt 1152
aacatatccc ctgtggttgg atatttgcta aacttcattg aacacccttg tagcagtttt 1212
tgtgcacatc tttttgtcaa ggcaaacttc ctagaagaga aattgctggc tcaaagggaa 1272
aaacagaata aatcgttttt tttatttcaa aaaaaaaaaa ccc 1315

<210> 261
<211> 1035
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> 98..673

<221> sig_peptide

<222> 98..376

<223> Von Heijne matrix

score 5.59999990463257

seq VLLLRQLFAQAEK/WY

<221> polyA_site

<222> 1025..1035

<400> 261

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aattttcylgt ggtccaacta ccctcggcga tcccaggctt ggccggggcac cgcctggcct 60
ctcccggtcc tttaggctgc cgccgctgcc tgccgcc atg gca gag ttg ggc cta 115
                                     Met Ala Glu Leu Gly Leu
                                     -90
aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt 163
Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg
      -85                                -80                                -75
tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac 211
Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp
      -70                                -65                                -60
ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc 259
Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val
      -55                                -50                                -45                                -40
tct gaa gtc ctc aat gga tta caa gct gtg gtt cat agt gag gtg gaa 307
Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu
                                     -35                                -30                                -25
tct gag ctc atc aac act gcc tat acc aat gtg tta ctt ctg cga cag 355
Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Leu Arg Gln
      -20                                -15                                -10
ctg ttt gca caa gct gag aag tgg tat ctt aag cta cag aca gac atc 403
Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile
      -5                                1                                5
tct gaa ctt gaa aac cga gaa tta tta gaa caa ktt gca gaa ttt gaa 451
Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu Gln Xaa Ala Glu Phe Glu
      10                                15                                20                                25
aaa gca rav att aca tct tca aac aaa aag ccc atc tta dat gtc aca 499
Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys Pro Ile Leu Xaa Val Thr
      30                                35                                40
aas cca aaa ctt gct cca ctt aat gaa ggt gga aca gca aaa ctc cta 547
Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly Gly Thr Ala Lys Leu Leu
      45                                50                                55
aac aag gta ata tgt att att ttg aga aac gga aag tct ctc att ctg 595
Asn Lys Val Ile Cys Ile Ile Leu Arg Asn Gly Lys Ser Leu Ile Leu
      60                                65                                70
tcc tgt cat tgc cta ggg tgg aga aac aaa agt gga agg ttt gtt tca 643
Ser Cys His Cys Leu Gly Trp Arg Asn Lys Ser Gly Arg Phe Val Ser
      75                                80                                85
ggt cct ctg agg ata att agt cca ttg cag tagttttact tgatggtacc 693
Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln
      90                                95
ccatggggcca gaagagggca tacttaacct tctagagagc ctgaagtagc tcctgatcac 753
acctttttcaa ggtaaaagtga agagcatgaa attttggaaca gcgtttattg atggacattt 813
aaagtttgtg atctgcggta acaaggagaa gggtttttaa gtttataaaa attatttatc 873
aattagccgg gtgtggtggt acgtgcctat agtcagagct actcgggagg ctgaggcagg 933

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agaattgctt gaacccggga ggtggaggtt gcagtgcgct gagatcacgc cactgcactc 993
tagcctgggc gacagagcga gactccatct caaaaaaaaa aa 1035

<210> 262
<211> 696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..463

<221> sig_peptide
<222> 17..232
<223> Von Heijne matrix
score 3.79999995231628
seq LMGLALAVYKCQS/MG

<221> polyA_signal
<222> 657..662

<221> polyA_site
<222> 684..696

<400> 262

actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act 52
Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr
-70 -65
atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc 100
Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro
60 -55 -50 -45
att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt 148
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser
-40 -35 -30
tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg 196
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu
-25 -20 -15
atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta 244
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu
-10 -5 1
cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga 292
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg
5 10 15 20
atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg 340
Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala
25 30 35
cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca 388
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro
40 45 50
gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac 436
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn
55 60 65
caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca 483
Gln Lys Thr Leu Phe Ser Met Val Gly
70 75

atgtgcatat	tacgacaaac	acaaaaaaaaac	tataccataa	cccagggctg	aaaataatgt	543
aaaaaaacttt	atttttgttt	ccagttacaga	gcaaaacaac	aacaaaaaaaa	cataactatg	603
taaacaaaaa	aataactgct	gctaaatcaa	aaactgttgc	agcatctcct	ttcaataaat	663
taaatgggtg	araacaatgc	aaaaaaaaaa	aaa			696

<210> 263
 <211> 868
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 263..481

<221> sig_peptide
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 <223> Von Heijne matrix
 score 11.1999998092651
 seq ILVVLMLPLAQA/LD

<221> polyA_site
 <222> 858..868

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ccaggagctcc	gggaggcagg gccggcccca cgtcctctgc gcaccacct gagttggatc 180
ctctgtgctgc	cacccttgag ttggatccag ggctagctgc tgttgacctc cccactccca 240
cgctgccctc	ctgcctgcag cc atg acg ccc ctg ctc acc ctg atc ctg gtg 292
	Met Thr Pro Leu Leu Thr Leu Ile Leu Val
	-20 -15
gtc ctc atg ggc tta cct ctg gcc cag gcc ttg gac tgc cac gtg tgt 340	
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys	
	-10 -5 1 5
gcc tac aac gga gac aac tgc ttc aac ccc atg cgc tgc ccg gct atg 388	
Ala Tyr Asn Gly Asp Asn Cys Phe Asn Pro Met Arg Cys Pro Ala Met	
	10 15 20
gtt gcc tac tgc atg acc acg cgc acc tac tac acc ccc acc agg atg 436	
Val Ala Tyr Cys Met Thr Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met	
	25 30 35
aag gtc agt aag tcc tgc gtg ccc cgc tgc ttc gar nac tgt gta 481	
Lys Val Ser Lys Ser Cys Val Pro Arg Cys Phe Glu Xaa Cys Val	
	40 45 50
tgatggctac	tccaagcacg cgtccaccac ctctgtctgc cagtacgacc tctgcaacgg 541
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gctayaccct	ckcaccckac tcaccctgcc tcaccctcca cactccttgc gacctectca 721
gccatgcccc	gggtcaggac tgtggggaag aagacacccg acctcccca accaccacac 781
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tgatgggctg	atcagcaaaa aaaaaaa 868

<210> 264
 <211> 775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 42..299

<221> sig_peptide

<222> 42..101

<223> Von Heijne matrix

score 5.40000009536743

seq WFWHSSALGLVLA/PP

<221> polyA_site

<222> 762..775

<400> 264

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Met Asn Leu His Phe

-20

cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca 104

Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro

-15 -10 -5 1 152

cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt

Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys

5 10 15 200

agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc

Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr

20 25 30 248

tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa

Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys

35 40 45 296

aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cgg

Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg

50 55 60 65 349

cag tgaaactwkk ttcwcttcta aagcccttca tttcccacaa ggттаagctc

Gln

tcgaaacccc atttgatcct tggttcctat ttcgatcctc ctttggaatc tgaaaatcgg 409

tctccatgtt gtatgcaaat taaaakttgc cttgtttgtt actcttccaa cacagggtat 469

cagggaraaa gaggccttat ctgttctctc atccccctg ttttgacaga ctgctaagaa 529

ttcctcagga cttccttttg ttggggattt tactttccca aaagtctgat ctgatttctt 589

tcaggggtag acaagcttgt cctagtgtc tgcttcaggt cttatcagaa gaaaccagg 649

aatagaaaag gtagatgcct tgacttttgt ccctgttgtg gggactaaag tgttttttgc 709

cagaattgtc aaaagctccg gttcaaaactc tgtagagttt catggaaaaa caaaacaaaa 769

aaaaaa 775

<210> 265

<211> 1075

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 198..431

<221> sig_peptide
 <222> 198..260
 <223> Von Heijne matrix
 score 6.90000009536743
 seq LLACGSLLPGLWQ/HL

<221> polyA_site
 <222> 1064..1074

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 agggactcag aagtcaaata gagtaggtta aaaacctctt atttttcaaa ttaattgttt 120
 taagaaacaa gcataacctgt gtaagtgaat tatcttaatt tgtgttgaat caagttagga 180
 gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc 230
 Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala
 -20 -15
 tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac 278
 Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His
 -10 -5 1 5
 tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca 326
 Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser
 10 15 20
 gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt 374
 Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg
 25 30 35
 tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac 422
 Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr
 40 45 50
 tct atc acc tagccattgt akccatacca agccgggctt cctacttccc 471
 Ser Ile Thr
 55
 tctgctcccc ttggtttcct cctgtraart aaatctcact gacccttgat gcasctccaa 531
 gcatatataa tatatatata ataaaacccat abtctaaaaa attcaaacca ggawaaataa 591
 asccaraaat ttgtatggga aaaatctgca caaatatttatt tggccagcat gggtatcatg 651
 gctctattga atttatcctt gaccgtcttt aaagccaaag caaacgggat aaagtgatca 711
 actacttacc tctcaatacc aaaaargaag caggaggcaa aatctctcaw taatttcata 771
 aaaaacaattc ttaktctgggc gcggtggctc wcacctgtar tcccaacact ttgggaggcc 831
 saggtgggcy gatcatgagg tcgggagatc aamaccatcc tggctaacat ggtgaaaccc 891
 catctctact aaaattacaa aaaatttrgct gggcgagggt gcgggcacct gtggtcccag 951
 ctactcggga ggctgaggca agagaatggg gtgaacccca gggggcggag cctgcagtga 1011
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 aaah 1075

<210> 266
 <211> 981
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 279..473

<221> sig_peptide
 <222> 279..362
 <223> Von Heijne matrix

score 4.40000009536743
seq SCFLVALIIWCYL/RE

<221> polyA_signal
<222> 944..949

<221> polyA_site
<222> 970..981

<400> 266

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cgctgaggct cataggctgg gcttcccgaa gccttcaccc gttgcccggg tcccgggatc      180
gggcccaccc tgccgccgag gaagaggacg accctgaccg cccattgag ttttctcca      240
gcaaagccaa ccctcaccgc tggtcggtgg gccatacc atg gga aag gga cat cag      296
                                Met Gly Lys Gly His Gln
                                -25
cgg ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg      344
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu
      -20                                -15                                -10
atc atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg      392
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu
      -5                                1                                5                                10
aga cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag      440
Arg Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu
                                15                                20                                25
cct gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg      493
Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
                                30                                35
ctggcaggaa gggagccgac asccgccctt cggatttgat ktcacgtttg cccgtgactg      553
tcctggctat gcktgctcc tcagcactra argacttggc tgggtggatgg ggcacttggc      613
tatgctgatt cgcgtgaagg cggavcaaaa tctcagcaaa tcggaaactg ctccctscct      673
ggctcttgat ktccaaggat tccatcggca aaacttctca ratccttggg gaaggtttca      733
gttgactgtg atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag      793
cacttctggt gacacttgct atccagtgtt agtttgcagg taatttgctt tctgagatag      853
aatatctggg agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc      913
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aaaaaaaaa

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<210> 267
<211> 1031
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 12..644

<221> sig_peptide
<222> 12..92
<223> Von Heijne matrix
score 4
seq LTFFSGVYGCIG/AT

<221> polyA_signal

<222> 1002..1007

<221> polyA_site

<222> 1020..1031

<400> 267

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          Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu
                    -25                    -20                    -15

gaa tta act ttc ttc tct ggt gta tat gga acc tgt att ggt gct aca      98
Glu Leu Thr Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr
                    -10                    -5                    1

aat aaa ttt gga gca gaa gag ara agc ctt att gga ctt tct ggc att      146
Asn Lys Phe Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile
                    5                    10                    15

ttc atc ggc att gga gaa att tta ggt gga agc ctc ttc ggc ctg ctg      194
Phe Ile Gly Ile Gly Glu Ile Leu Gly Gly Ser Leu Phe Gly Leu Leu
                    20                    25                    30

agc aag aac aat cgt ttt ggt aga aat cca gtt gtg ctg ttg ggc atc      242
Ser Lys Asn Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile
                    35                    40                    45                    50

ctg gtg cac ttc ata gct ttt tat cta ata ttt ctc aac atg cct gga      290
Leu Val His Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly
                    55                    60                    65

gat gcc ccg att gct cct gtt aaa gga act gac agc agt gct tac atc      338
Asp Ala Pro Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile
                    70                    75                    80

aaa tcc agc aaa raa ttt gcc att ctc tgc akt ttt ctg tkg ggc ctt      386
Lys Ser Ser Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu
                    85                    90                    95

gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg      434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu
                    100                   105                   110

tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag      482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln
                    115                   120                   125                   130

act att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctc ctt      530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu Leu
                    135                   140                   145

cac tgg caa ctc ctg gtc atg gtk atw ttt ggg ttt ttk gga aca att      578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile
                    150                   155                   160

tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc ggc      626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly
                    165                   170                   175

tct gac tac cga agt atc tgatctggtg tccgtgaggg gacacgtatg      674
Ser Asp Tyr Arg Ser Ile
                    180

acctcagaaa cacagctgga cacagagctt ggtggaagaa gtcgcctttg atcttcacta      734
tatattgggt gatgttcagt atggaaaatc aagggattaa gactgttaaa tcagccagag      794
tkggtgttca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctgtt      854
ctgtcaactg taattgttca aagatgttgt ttttcatttc atctatctca attcttataa      914
tcattgttata gaattgaaat gttttcttct ctctcctgct cttgttgga gacacctgct      974
tgatttagaa tactaggcca tatgtcatat aaatatTTTT tctggaaaaa aaaaaaaa     1031

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<210> 268
 <211> 1283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..459

<221> sig_peptide
 <222> 91..330
 <223> Von Heijne matrix
 score 7.69999980926514
 seq LVLFLSLALLVTP/TS

<221> polyA_site
 <222> 1271..1281

<400> 268
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 ttgccctata ttcgtgttga gggttcacac atg agc aca tgg tat ttg gca ctt 114
 Met Ser Thr Trp Tyr Leu Ala Leu
 -80 -75
 aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctc agc ttg 162
 Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu
 -70 -65 -60
 tgc aca gtg agc att aaa ttt aca tac ttt cat gat ata cag act aat 210
 Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn
 -55 -50 -45
 tgt ctt aca aca tgg aaa cat tcg aga tgc aga ttt tat tgg gca ttt 258
 Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe
 -40 -35 -30 -25
 ggt ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta 306
 Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Leu Phe Leu
 -20 -15 -10
 agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata 354
 Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile
 -5 1 5
 car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac 402
 Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp
 10 15 20
 agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt 450
 Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu
 25 30 35 40
 cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct 499
 His Gln Leu
 gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaaag 559
 ctattaagtt attaagtgtc agccctggat cttggcttat tgtgaaatgt taattatttt 619
 atcactcyat taagaagctg tgggctccat ctccagcattg aaaagggact aatttgctct 679
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 ctctactaaa aatacaaaaar aattakccgg gcatggtagt gggcgccctgt gtaccagct 1159

actggggagg	ctgaggcarg	araatcgctt	gaacctggga	ggcggagggtt	gcastragct	1219
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aamc						1283

<210> 269
 <211> 1777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..327

<221> sig_peptide
 <222> 70..147
 <223> Von Heijne matrix
 score 9.60000038146973
 seq WLIALASWSWALC/RI

<221> polyA_signal
 <222> 1741..1746
 <221> polyA_site
 <222> 1763..1774

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Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp	
-25 -20 -15	
cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt	159
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu	
-10 -5 1	
tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt	207
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Ile Ile Leu Leu	
5 10 15 20	
ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat	255
Leu Leu Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp	
25 30 35	
gta ttg ctt tat ttt ccw kaa cag yya tcc tct tca cgt ctt tat gat	303
Val Leu Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp	
40 45 50	
tcc cat gcc cac tgg cmt tcg rca taaaaaaaaatt ttcattcagaa ccaaagatgg	357
Ser His Ala His Trp Xaa Ser Xaa	
55 60	
aatacgtctg aatcttattt tgatacgata cactggagac aattcaccct attccccaac	417
tataatttat tttcatggga atgcaggcaa cataggtcac aggttggcca aatgcattac	477
ttatgttgggt taacctcaaa gttaaccttt tgctggttga ttatcgagga tatggaaaaa	537
gtgaaggaga agcaagtga gaaggactct acttagattc tgaagctgtg ttagactacg	597
tgatgactag acctgacctt gataaaaacaa aaatttttct ttttggccgt tccttgggtg	657
garcagtggc tattcatttg gcttctgaaa attcacatag gatttcagcc attatggtgg	717
agaacacatt tttaagcata ccacatatgg ccagcacttt attttcattc tttccgatgc	777
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<210> 270

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..497

<221> sig_peptide

<222> 12..104

<223> Von Heijne matrix

score 5.5

seq LVGVLFVFSVTTG/PW

<221> polyA_signal

<222> 935..940

<221> polyA_site

<222> 955..967

<400> 270

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          -30                      -25                      -20

gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act 98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
          -15                      -10                      -5

aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg 146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
          1                      5                      10

ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca 194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
          15                      20                      25                      30

aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca 242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
          35                      40                      45

gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc 290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser
          50                      55                      60

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agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
      65                      70                      75
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser
      80                      85                      90
cat gtc tct ttt tct tgg atg gtt ggg agc aga tgc att tta cct tgg      434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
      95                      100                      105                      110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg      482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp
      115                      120                      125
aat tgg gag cct aat tgatttcaty cttatttcaa tgcagattgt tggaccttca      537
Asn Trp Glu Pro Asn
      130
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact      597
aatgaaacat ttagaaaaaac gcaattatat ccataaatat tttttaaag aaacagattt      657
gagcctcctt gattttaata gagaacttct agtgtatgga tttaaagatt tctctttttc      717
attcatatac cattttatga gttctgtata attttttgtg gtttttggtt tggtgagtta      777
aagtataata ttgtgagatt tatttaaatg gacttccttt gaaagctgta taatagtgtt      837
tctcgggctt ctgtctctat gagagatagc ttattactct gatactcttt aatcttttac      897
aaaggcaagt tgccacttgt cattttttgtt tctgaaaaat aaaagtataa cttattcaca      957
aaaaaaaaaa mms                                                    970

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<210> 271

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 90..383

<221> sig_peptide

<222> 90..200

<223> Von Heijne matrix

score 4.90000009536743

seq MLIMLGIFNVHS/AV

<221> polyA_signal

<222> 609..614

<221> polyA_site

<222> 632..643

<400> 271

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atctctgccc ccctgcgagg gcatcctggg ctttctccca ccgctttccg agcccgttg      60
cacctcggcg atccccgact cccttcttt atg gcg tgc ctc ctg tgc tgt ggg      113
                                Met Ala Ser Leu Leu Cys Cys Gly
                                -35                      -30
ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc      161
Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile
      -25                      -20                      -15
atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg      209
Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu

```

	-10		-5		1	
att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car						257
Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln						
5		10		15		
aac ata tac aac ctt tac rag caa ktc agc tac aac tgt ttc atc gct						305
Asn Ile Tyr Asn Leu Tyr Xaa Gln Xaa Ser Tyr Asn Cys Phe Ile Ala						
20		25		30		35
gca ggc ctt tac ctc ctc ctc gga ggc ttc tct ttc tgc caa ktt cgg						353
Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Xaa Arg						
	40		45		50	
ctc aat aag cgc aag gaa tac atg gtg cgc tagggccccc gcgcgtttcc						403
Leu Asn Lys Arg Lys Glu Tyr Met Val Arg						
	55		60			
ccgctccagc ccttcctcta tttaaact cctgcaccg tktcacccag gtcgcgtccc						463
acccttgccg gcgccctctg tgggactggg tttcccgggc rararactga atcccttctc						523
ccatctctgg catccggccc ccgtggarar ggctgaggct ggggggctgt tccgtctctc						583
cacccttcgc tgtgtcccg atctcaataa agagaatctg ctctcttcaa aaaaaaaaaa						643
my						645

<210> 272
 <211> 773
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..541

<221> sig_peptide
 <222> 332..376
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FLPCCLLWSVFPN/ES

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 761..773

<400> 272	
aaaacaattc atgcctttca tagtttatta ttattaaagt ctaaacaaaa ttgcaatttc	60
ttaggtaacc ttatatattac aataaatgaa gattaccctc aaatgctaga agctgtctag	120
gtccgtccgg tgtgtcagat tttcctcaga ttagatgtgc caataaccaa gtttattcag	180
taaacaactt gtacttgttt catctggttt tattactctc acccataaac agtaatgact	240
ctctgaccct ctggaaatat gtaatgcttc caatcttgct ttgtgtatct catttaattt	300
gttataaggt agtactgatt ttagcatatt a atg cga ttt ctt cct tgt tgt	352
	Met Arg Phe Leu Pro Cys Cys
	-15 -10
ttg ctt tgg tct gtg ttc aat cca gag agc tta aat tgt cat tat ttt	400
Leu Leu Trp Ser Val Phe Asn Pro Glu Ser Leu Asn Cys His Tyr Phe	
	-5 1 5
ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca	448
Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser	
10 15 20	

```

ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac      496
Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr
25                      30                      35                      40
ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act      541
Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr
                      45                      50                      55
tgaaaagaaa gtgttttatt ttcaaactctg gtccatattt acattctagt tcagagccaa      601
gccttaaaact gtacagaatt tccactgtaa ttaaaactat ttagtgtagg ttataaatag      661
ccttcaaaaa gagagattct ccattacacg atcacctgca tcacagccca tggatgaatgt      721
atgtttctgc atagcgaaat aaaaatggca aatgcactga aaaaaaaaaa aa      773

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<210> 273
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..222

<221> sig_peptide
 <222> 43..177
 <223> Von Heijne matrix
 score 4
 seq ENFLSLLSKSCSA/DP

<221> polyA_signal
 <222> 530..535

<221> polyA_site
 <222> 555..566

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<400> 273
aacgagtggg ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt      54
                                   Met His Ser Leu
                                   -45
ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg      102
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg
-40                      -35                      -30
ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt      150
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu
-25                      -20                      -15                      -10
agc ctt ctc agc aaa agt tgt tct gcg gac ccg tct ggg tca act ttc      198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe
                      -5                      1                      5
atg agg gac att gag aca aac aaa tgaaatatgg gttaaagtac tctgagcagc      252
Met Arg Asp Ile Glu Thr Asn Lys
10                      15
tacaaaaaga araccagtct atcctgctgg agacagtggc cacgtgaara aagagctctt      312
gcagtatgaa agaccacatg gaaagagagg ccacatggaa ccaacagtca gcattctggg      372
ttcggacacg tgaaraaatt catctcarac tgtgtatcct aaatcaggca cttgctgaat      432
ctaactacat gagtgagacc agttgacaac acatggagca racatgagct gttctcagt      492
artcctacat aaattcctga ctcacaacac tgtgagcaat aaaatggttg ttattttaag      552
ccaaaaaaaa aaaa      566

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<210> 274
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..231

<221> sig_peptide
<222> 115..180
<223> Von Heijne matrix
score 5
seq HLFVTWSSQRALS/HP

<221> polyA_signal
<222> 419..424

<221> polyA_site
<222> 445..455

<400> 274
aacctgccag tkatgcaaat gccaaaatgt gggatcatcat atagtatatatt tgaaaccttt 60
Ctgaacatgt acaccaccca atgctagagg ctgacttgga aaccggtggg tgca atg 117
Met
ccc gag gct gtg gaa caa tca gcc cat ctc ttt gtg acc tgg agc agt 165
Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser Ser
-20 -15 -10
cag agg gcc ctc agt cac ccc gcc cca ttc ctc acc ara raa aar aat 213
Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys Asn
-5 1 5 10
cca ttt cta tgg aag ctc tgacgtaact tcagtgtttt ctacaataact 261
Pro Phe Leu Trp Lys Leu
15
ccctcctgccc cgccccatta aaacagttct tttgttaaaa aatavcctaa tgggtccaact 321
attgtgtgtctg ttctttccaaa tgtttataat acacattatt tataaatatg tctgtttggg 381
aagctaagaa caagctagtt tttaacaacac aaatggaaat aaatgcaatt attataaaaa 441
tycaaaaaaa aaaa 455

<210> 275
<211> 673
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 232..384

<221> sig_peptide
<222> 232..300
<223> Von Heijne matrix
score 3.70000004768372
seq FFLCAAFPLGAGV/KM

<221> polyA_signal
<222> 650..655

<221> polyA_site
<222> 662..673

<400> 275
at ttg gct t g cag act g c c t t c t a t c c c a g a a c a g c t g a g a a a t c t a t g a a g c t g a g a t t 60
c t g a a g g a c c c a g c t t a g g t t c t t c c a c t t a g g c c t c a a t t c c c t t c c t t t c c a g g g g c 120
a g c c t t a g t t t c c a t g g c c t g a a a c a c a c a c a t t t c c c c c t t c c t t t c c a g a a g c c a 180
c t g g c c c c c c a t a g c a c c c a g t g c a t c c t t t t a c a a g t g g a a g a a c t a g g a t g g c t 237
Met Ala
t t c c a a a g t c t t c t a g a a a t g a a g t t c t t t c t c t g t g c a g c t t t c c c 285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro
-20 -15 -10
c t t g g a g c a g g a g t g a a g a t g t t t c a t t a t c t t g g g c c t g g g a a a c c a 333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro
-5 1 5 10
c t t c y y c a g g c t t c t c c c t c c c c a c c c c a t a g g a m c a g g a t t t g g 381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp
15 20 25
c c t t a g c t t c t g g g c c t a t c s g c t g c c t t c c c t c t t y t t c c t a c c a c c t c t t c 434
Pro
t g c c t t c c c t t t r a w c t c t g t t g g g c t t g g g g a t c t t a g t t t t c t t t t g t t t a t t t c c c a t 494
c t c a t t t t t t t c t t t c t g g t c a g t t t t t t t a a g g g g g g t g t t g t g g t t t t t g t t t t t g t 554
t t t g c t t c t g a a a a a r c a t t t g c c t t t c c t c c t c c c a a c a t a a c a a t c g t g g t a a c a g 614
a a t g c g a c t g c t g a t t t a c c g a t g t a t t t a a t g t a a g t a a a a a a g g a a a a a a r a a a a 673

<210> 276
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..427

<221> sig_peptide
<222> 143..286
<223> Von Heijne matrix
score 7.5
seq FVILLLFIFTVVS/LV

<221> polyA_signal
<222> 606..611

<221> polyA_site
<222> 628..639

<400> 276
a a t c g c t t c a g c a g c a t c c t c t c a g a c a a g a g c c a c t a t t t c t g a t t c a g a t c a c c t g t c 60
a t c g a a g t t t a a a g a a g g g g a a a c a g g a g a c a g a a a t a c a c t g a a c c a a a a a g a t t c a a a 120
a g a g c a a g t g g a a t c t c t a a g a a t g g c t c c a g c c a c t g g a a t g a a a c c a c t 172
Met Ala Ser Ser His Trp Asn Glu Thr Thr

$\langle 210 \rangle$ 277

<211> 772

212 DNA

<213> Homo sapiens

<220>

221 CDS

$\langle 222 \rangle$ 284..463

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<221> sig_peptide
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$\langle 222 \rangle$ 284..379

<223> Von Heijne matrix

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score 3.79999995231628
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seq TFINITLWLGSLC/QR

<221> polyA_site

<222> 762..772

<400> 277

acagctgggg ctttgtcttc tttattgcta ggagaatgta gcaatagaag ttctcatcgc 60

cctgtattgc acttttgggt ttaaggactg gaccagagt tcctgaaagc caaactccat 120

aagctgctca gtaagttcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct 180

gttgaatgaa ggtagacgca gcaggcagtt tgtccttacc agtgacctgg aagacggtgg 240

cacttcctga gtgagctcac ttaccttccc tgaatggtga ggc atg gat gaa tat 295

Met Asp Glu Tyr

-30

tcc tgg tgg tgc cac gtg tta gag gtg gta aag ggt caa atg ttt act 343

Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly Gln Met Phe Thr

-25

-20

- 15

ttt att aat att aca tta tgg ctt ggt tct ctg tgt cag cga ttt ttc 391

Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys Gln Arg Phe Phe

-10

-5

1

tat gcc tcg ggt act	tat ttc cta ata tat atc agc aca gta acg cct	439
Tyr Ala Ser Gly Thr	Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro	
5	10 15 20	
agc tgg agg ctt tgt ctt gtt agt	tgataaatta gtggtaacag gtagatttgg	493
Ser Trp Arg Leu Cys Leu Val Ser		
25		
ttacctccca aagtgtctggg atttcagacg	tgagccaccg cgcttgccg aaacaattct	553
tttgaaagag agaagctctc ctgtgttgcg	caggctgggc tcagactcct ggggtcaagt	613
gagctcctg ctttcgcctc ctaaagtgtc	gggattacag gcgtgagcca ccgacccgg	673
acagatgtgt tgattttaaa gtgggtatga	ggcctgagcc ctggagtttg agaccagcct	733
ggacaacatg gcaagaccct gtctctccaa	aaaaaaaaa	772

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<210> 278
<211> 840
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 162..671
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```
<221> sig_peptide
<222> 162..398
<223> Von Heijne matrix
score 4.09999990463257
seq QGVLFICFTCARS/FP
```

```
>>> polyA_signal
805..810
```

```
<221> polyA_site
<222> 830..840
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<400> 278

1	caaaaaactgag	gctctgggagc	aggaacctgt	aggcagcgct	tgagggtagc	gggatagcag	60
2	ctgcaacgcg	cgtgggaggc	gggggctctg	ggcggaacaa	aatcacagg	atgtcagagg	120
3	atgtttcccg	ggaagaactg	ggataaaggg	gtcccagcac	c atg gag gac ccg aac		176
					Met Glu Asp Pro Asn		
					-75		

cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc 224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
-70 -65 -60

cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc 272
Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr
-55 -50 -45

cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg 320
 Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met
 -40 -35 -30

aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc 368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val
-25 -20 -15

ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa gcc 416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala
-10 -5 1 5

ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg 464

Xaa	Xaa	Thr	His	Gln	Arg	Ser	His	Gly	Pro	Xaa	Ala	Lys	Pro	Thr	Leu	
			10					15					20			
ccg	gtt	gca	acc	act	act	gcc	car	ccc	acc	ttc	cct	tgt	cct	gac	tgt	512
Pro	Val	Ala	Thr	Thr	Thr	Ala	Gln	Pro	Thr	Phe	Pro	Cys	Pro	Asp	Cys	
		25					30				35					
ggc	aaa	acc	ttt	ggg	cag	gct	gtt	tct	ctg	arg	cgg	cac	csc	caa	atr	560
Gly	Lys	Thr	Phe	Gly	Gln	Ala	Val	Ser	Leu	Xaa	Arg	His	Xaa	Gln	Xaa	
	40					45					50					
cat	gar	gtc	cgt	gcc	cct	cct	ggc	acc	ttc	gcc	tgc	aca	rad	tgc	ggg	608
His	Glu	Val	Arg	Ala	Pro	Pro	Gly	Thr	Phe	Ala	Cys	Thr	Xaa	Cys	Gly	
55					60					65				70		
cag	gac	ttt	gct	car	gaa	rca	ggg	ctg	cat	caa	cac	tac	att	cgg	cat	656
Gln	Asp	Phe	Ala	Gln	Glu	Xaa	Gly	Leu	His	Gln	His	Tyr	Ile	Arg	His	
			75					80				85				
gcc	cgg	ggg	gga	ctc	tgagttcagc	ttaagcctct	ccacggtgac	gggtggctct								711
Ala	Arg	Gly	Gly	Leu												
			90													
gtggctggta	ggactcacc	atgatatggg	gtgcaggaac	tctggggggc	ctgaaggatt											771
tgcttccctc	ccctgggaag	gcagagggct	cttaataaag	aggaccbaka	agattcttaa											831
aaaaaaaa																840

<210> 279
 <211> 840
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 :: <222> 63..632
 <221> sig_peptide
 <222> 63..308
 <223> Von Heijne matrix
 score 4.40000009536743
 seq NLPHLQVVGLTWG/HI

<221> polyA_signal
 <222> 808..813

<221> polyA_site
 <222> 829..840

<400>	279															
aacttcggt	cgcgccascg	cccgttgcc	gttctgcgcg	tgtcctgcat	ctccagtatg											60
ga	atg	tat	gtd	tgg	ccc	tgt	gct	gtg	gtc	ctg	gcc	cag	tac	ctt	tgg	107
Met	Tyr	Val	Trp	Pro	Cys	Ala	Val	Val	Leu	Ala	Gln	Tyr	Leu	Trp		
	-80						-75					-70				
ttt	cac	aga	aga	tct	ctg	cca	ggc	aag	gcc	atc	tta	gag	att	gga	gct	155
Phe	His	Arg	Arg	Ser	Leu	Pro	Gly	Lys	Ala	Ile	Leu	Glu	Ile	Gly	Ala	
	-65						-60					-55				
gga	gtg	agc	ctt	cca	gga	att	ttg	gct	gcc	aaa	tgt	ggt	gca	gaa	gta	203
Gly	Val	Ser	Leu	Pro	Gly	Ile	Leu	Ala	Ala	Lys	Cys	Gly	Ala	Glu	Val	
	-50					-45					-40					
ata	ctg	tca	gac	agc	tca	gaa	ctg	cct	cac	tgt	ctg	gaa	gtc	tgt	cgg	251
Ile	Leu	Ser	Asp	Ser	Ser	Glu	Leu	Pro	His	Cys	Leu	Glu	Val	Cys	Arg	

-35	-30	-25	-20	
caa agc tgc caa atg aat aac ctg cca cat ctg cag gtg gta gga cta				299
Gln Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu				
	-15	-10	-5	
aca tgg ggt cat ata tct tgg gat ctt ctg gct cta cca cca caa gat				347
Thr Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp				
	1	5	10	
att atc ctt gca tct gat gtg ttc ttt gaa cca gaa rat ttt gaa gac				395
Ile Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp				
	15	20	25	
att ttg gct aca ata tat ttt ttg atg cac aar aat ccc aag gtc caa				443
Ile Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln				
	30	35	40	45
ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct				491
Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala				
	50	55	60	
tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct				539
Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser				
	65	70	75	
ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga				587
Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg				
	80	85	90	
cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc				632
His Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu				
	95	100	105	
tgaaattatac ctacaacctg ttctgggaca gtatcaatac tgatgagcaa cctggcacac				692
aaactatgag cagaccactt cagcttgaga atgcagtggg tctgaagatg gtcaagtctg				752
tttgccttar attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa				812
aatatcgatt acaagcaaaa aaaaaaaaa				840

<210> 280
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..362

<221> sig_peptide
 <222> 21..200
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LVILSLKSQTLDA/ET

<221> polyA_signal
 <222> 821..826

<221> polyA_site
 <222> 838..849

<400> 280
 agtaagtccc cccgcctcgc atg atg gct gcg gtg ccg ccg ggc ctg gag ccg 53
 Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
 -60 -55 -50

tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca	101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr	
-45 -40 -35	
gtg cag aac ccc gcc gcg gcc ctt gac ctt tgc att gca gct gta att	149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile	
-30 -25 -20	
aaa gaa tgc cat ctc gtc ata ctg tcg ctg aag agc caa acc tta gat	197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp	
-15 -10 -5	
gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga	245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg	
1 5 10 15	
atg gcc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt	293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys	
20 25 30	
tta aag cgt ttg aaa aac atg aat ttg gag gcc tca att caa gac ctg	341
Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu	
35 40 45	
ttt gag ttg ttt tct tcc aag taagtaagtg gtccarttgc tttgtgatgt	392
Phe Glu Leu Phe Ser Ser Lys	

50

gggtgggctgg gaactcaatg tcttgtgatc kcccttwgga tktctctakg ctygckgttg	452
gaatataacc aattataaccw cagctgtaka aatwttgttt taatgtgggg taccygggtg	512
ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt	572
catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga	632
gcttaaagca agtcttcact tgaaaaactgc tatagaaatg ctttataattt aaaaatgaaa	692
gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc	752
tctgtgcttc ttctgccata ccttgcccta tgcattctctt tgtttcaatc ctttgtcata	812
tcctttataa taaactggta aatgtaaaaa aaaaaaa	849

<210> 281

<211> 1344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..503

<221> sig_peptide

<222> 21..344

<223> Von Heijne matrix

score 5.30000019073486

seq ACMTLTASPGVFP/SL

<221> polyA_signal

<222> 1305..1310

<221> polyA_site

<222> 1330..1341

<400> 281

aaacaactcc ggaaagtaca atg acc agc ggg cag gcc cga gct tcc wyc cag	53
Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln	

-105

-100

tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca	101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser	
-95 -90 -85	
atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc	149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg	
-80 -75 -70	
aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt	197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu	
-65 -60 -55 -50	
tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct	245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro	
-45 -40 -35	
aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag	293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln	
-30 -25 -20	
gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc	341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe	
-15 -10 -5	
ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg	389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr	
1 5 10 15	
cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa	437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln	
20 25 30	
aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg	485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu	
35 40 45	
gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag	533
Glu Lys Ser Ile Met Leu	
50	
atgatgaccg ttcattaata aatttgcac tcacgacac cagttacttc ctctttgtga	593
tggtgataac aatgttttgc tatgctgtta tcaagggcag acctagcaaa ttgcgtcaga	653
gcaatcctga attttgtccc gagaagggtg ctttggctga agcctaattc cacagctcct	713
tgttttttga gagagactga gagaaccata atccttgcc tctgaaccca gctgggcct	773
ggatgctctg tgaatacatt atcttgcat gttgggttat tccagccaaa gacatttcaa	833
gtgcctgtaa ctgatttgta catatttata aaaatctatt cagaaattgg tccaataatg	893
cacgtgcttt gccctgggta cagccagagc ccttcaaccc caccttggac ttgaggacct	953
acctgatggg acgtttccac gtgtctctag agaaggatcc tggatctagc tggtcacgac	1013
gatgttttca ccaaggtcac aggagcattg cgtcgtgat ggggttgaag tttggtttgg	1073
ttcttgtttc agcccaatat gtagagaaca tttgaaacag tctgcacct tgatacggta	1133
ttgcatttcc aaagccacca atccattttg tggattttat gtgtctgtgg cttaataatc	1193
atagtaacaa caataatacc tttttctcca ttttgcttgc aggaaacata ccttaagttt	1253
tttttgtttt gtttttgttt ttttgttttt tgttttcctt tatgaagaaa aaataaaata	1313
gtcacatttt aatacyaaaa aaaaaaaamc h	1344

<210> 282
 <211> 671
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..201

<221> sig_peptide

<222> 1..63

<223> Von Heijne matrix
score 5.09999990463257
seq LLLKIWLLQRPES/QE

<221> polyA_signal

<222> 637..642

<221> polyA_site

<222> 660..671

<400> 282

atg ctg gga ggt gac cat agg gct ctg ctt tta aag ata tgg ctg ctt	48
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu	
-20 -15 -10	
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg	96
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val	
-5 1 5 10	
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt	144
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val	
15 20 25	
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca	192
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro	
30 35 40	
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtctttgg	241
Leu Arg Met	
45	
ctcagttcat ttaaaaaaga tatctatttg aaagttctca rarttgtaca tatgtttcac	301
agtacaggat ctgtacataa aagtttcttt cctaaacat tcaccaagag ccaatatcta	361
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtcctc cttgttattt	421
ctgtttgtaa racttaagtg agttaggtct ttaaggaaaag caacgctcct ctgaaatgct	481
tgctcttttt ctgttgccga aatarctggt cctttttcgg gagttaratg tatarartgt	541
ttgtatgtaa acatttcttg taggcacac catgaacaaa gatatatattt ctatttattt	601
attatatgtg cacttcaaga agtcactgtc agagaaataa agaattgtct taaatgtcaa	661
aaaaaaaaaa	671

<210> 283

<211> 1601

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..1034

<221> sig_peptide

<222> 39..134

<223> Von Heijne matrix
score 6.09999990463257
seq LPLLTSALHGLQQ/QH

<221> polyA_signal

<222> 1566..1571

<221> polyA_site

<222> 1587..1597

<400> 283

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agccccagat cctgaaggag gtgcagagcc cagagggg atg atc kcg ctg agg gac      56
                               Met Ile Xaa Leu Arg Asp
                               -30
aca gct gcc tcc ctc cgc ctt gag aga gac aca agg cag ttg cca ctg      104
Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu
-25 -20 -15
ctc acc agt gcc ctg cac gga ctg cag cag cag cac cca gcc ttc tct      152
Leu Thr Ser Ala Leu His Gly Leu Gln Gln Gln His Pro Ala Phe Ser
-10 -5 1 5
ggg gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt      200
Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly
10 15 20
gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc      248
Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Leu Phe
25 30 35
ctg cac cct gag ccc ttc acc cct ccg agt tcc ccc cag gtt ggc ttc      296
Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe
40 45 50
ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc      344
Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro
55 60 65 70
ctc ttt gtc aac ctc aat aat gag ctc act gtg gag gag cag gtg gar      392
Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu
75 80 85
atc cgc agt ggc ttc ctg gca gct cgg gca cag ctc ccc gtc atg gtc      440
Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val
90 95 100
att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga      488
Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly
105 110 115
ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc      536
Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa
120 125 130
ctg ccc atg tta rar aas cag ctc atg gat ccc cgg gga cct ggg gac      584
Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp
135 140 145 150
atc agg aca gkg ttc cgg ccg ccc ttg gac att tac gac gtg ctg att      632
Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile
155 160 165
cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr      680
Arg Leu Ser Pro Arg His Ile Pro Arg His Arg Gln Ala Val Asp Ser
170 175 180
cca gct gcc tcc ttc tgc cgg ggc ctg ctc agc cag ccg ggg ccc tca      728
Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu Ser Gln Pro Gly Pro Ser
185 190 195
tcc ctg atg ccc gtg ctg ggc tak gat cct cct cag ctc tat ctg acg      776
Ser Leu Met Pro Val Leu Gly Xaa Asp Pro Pro Gln Leu Tyr Leu Thr
200 205 210
cag ctc arg gag gcc ttt ggg gat ctg gcc ctt ttc ttc tat gac cag      824
Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala Leu Phe Phe Tyr Asp Gln
215 220 225 230
cat ggt gga gag gtg att ggt gtc ctc tgg aag ccc acc agc ttc cag      872
His Gly Gly Glu Val Ile Gly Val Leu Trp Lys Pro Thr Ser Phe Gln
235 240 245

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ccg cag ccc ttc aag gcc tcc agc aca aag ggg cgc atg gtg atg tct      920
Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys Gly Arg Met Val Met Ser
          250                      255                      260
cga ggt ggg gag cta gta atg gtg ccc aat gtt gaa gca atc ctg gag      968
Arg Gly Gly Glu Leu Val Met Val Pro Asn Val Glu Ala Ile Leu Glu
          265                      270                      275
gac ttt gct gtg ctg ggt gaa ggc ctg gtg cag act gtg gag gcc cga      1016
Asp Phe Ala Val Leu Gly Glu Gly Leu Val Gln Thr Val Glu Ala Arg
          280                      285                      290
agt gag agg tgg act gtg tgatcccagc tctggagcaa gctgtagacg      1064
Ser Glu Arg Trp Thr Val
          295                      300
gacagcagga cattggacct ctagagcaag atgtcagtag gatgacctcc accctccttg      1124
gacatgaatc ctccatggag ggctgtctgg ctgaacatgc tgaatcatct ccaacaaaac      1184
ccagcccaaa ctttctctct gatgctccag cattgggggca ggggcatggt ggcccatgta      1244
gtctcctggg cctcaccatc ccagaagagg agtgggagcc agctcagaga aggaactgaa      1304
cccaggagat ccatccacct attagccctg ggcttgacc tccctgcgat ttccactcc      1364
tttcttagtc ttcttcacaga aacagagaag gggatgtgtg cctgggagag gctctgtctc      1424
cttcctgtcg ccaggacctg tgcctagact tagcatgcc ttcactgcag tgtcaggcct      1484
ttagatggga cccagcgaaa atgtggccct tctgagtcac atcaccgaca ctgagcagtg      1544
gaaaggggct atatgtgtat gaatagacca cattgaagga gcaaaaaaaaa aaamcch      1601

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<210> 284
<211> 1206
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 69..263
<221> sig_peptide
<222> 69..125
<223> Von Heijne matrix
score 3.90000009536743
seq ALSMSSFSFHSSS/CS

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<221> polyA_signal
<222> 1173..1178

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<221> polyA_site
<222> 1196..1205

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<400> 284
acatttgatga ctttaccaat accctcccag ttcttgatag acagctgtag gttgctgggt      60
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt      110
          Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser
                    -15                      -10
ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc      158
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser
-5                      1                      5                      10
aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta      206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu
          15                      20                      25
gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa      254

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Glu	Asn	Ala	Ser	Leu	Pro	Phe	Pro	His	Leu	Gly	Ser	Ser	Leu	Phe	Lys	
30							35				40					
att	gtg	ggc	tgatt	tggtc	ttcct	ctcct	cctccc	actg	ttact	gccct						303
Ile	Val	Gly														
45																
gcagcc	cttg	ttcag	gtgta	cagacc	ctta	ttctg	gcctc	tagt	gtcctt	gtct	gtcatg					363
acacacc	ctt	ccgccc	aaat	acctct	gacc	ccaagg	ctgg	aatg	gggctg	gtag	garata					423
agtttg	ctta	ctcatart	ca	tgccct	ttct	cttg	gcacct	gctt	ccctgc	ggtg	tcctca					483
aatgg	atttc	tgtgtg	gcag	tggart	gatt	gcat	gaattt	ttct	gtaaca	catta	actttt					543
gtattatt	at	taagg	gartt	tgaraa	agct	ttgctt	tataa	tgtca	aggca	aggag	gtaaa					603
aactgg	agcc	caaakaa	aatt	cccttag	ggc	aagatt	atgt	tataa	ataraa	aattg	aattt					663
cctgag	gcag	tggctg	ccac	ccctttt	car	atgttt	tagtc	ctgca	aata	catctt	tctt					723
gtagtct	gtg	acatg	gatgg	ggatg	ctagg	gccctt	taggg	gcaag	gggac	taaact	aaaat					783
caaktt	gagt	tttttt	ccag	cagggg	ttar	gggag	gtact	csctg	ttgat	atttg	acact					843
araaag	taat	ctttttt	taca	aaactg	tttt	tctag	gtggg	tggaa	agtga	aactg	gccaca					903
tccttg	ttg	tttagt	ccaa	raratc	attt	gcaaca	acag	tarat	gtccg	ggtttt	gttt					963
ctgtct	tttt	attatg	aaaaa	actatg	ttaa	ggggg	aaaat	gtgg	attatg	gtaacc	arag					1023
gaatcc	ctas	ccttg	ttttc	cttara	arac	ttgtt	tagtg	ttttat	cara	cgtct	gttgt					1083
agttg	tarac	aggaa	agctt	gtgara	aaaaa	caccac	atgg	ascct	gtaaa	tgtttt	tgca					1143
caacct	gtaa	agcatt	cttg	gaaktg	ggcca	gtaaaa	aggg	gtttt	accat	ttaaaaaa	aat					1203
aat																1206

<210> 285
 <211> 536
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 115..285
 <221> sig_peptide
 <222> 115..204
 <223> Von Heijne matrix
 score 3.70000004768372
 seq SMLLLTVYGGYLC/SV

<221> polyA_signal
 <222> 505..510

<221> polyA_site
 <222> 525..536

<400> 285	
acgagt	gctg
cggttc	ggctg
tgctg	ggaag
ttgcg	tagac
agtg	gcctcg
agacc	ctgcc
tgctg	agga
ggcctc	gggtt
ggatg	cgaag
gagct	gcagc
atccag	ggga
caag	atg
	Met
	-30
cca act	ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc
Pro Thr	Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr
	-25 -20 -15
tcc atg	atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga
Ser Met	Met Leu Leu Thr Val Tyr Gly Gly Tyr Leu Cys Ser Val Arg
	-10 -5 1
gtc tac	cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa
	261

Val	Tyr	His	Tyr	Phe	Gln	Trp	Arg	Arg	Ala	Gln	Arg	Gln	Ala	Ala	Glu	
5						10					15					
gaa cag aag dac tca gga atc atg tagaactggg gggctttttc tcctgagcar																315
Glu	Gln	Lys	Xaa	Ser	Gly	Ile	Met									
20					25											
asakgcccac ggcattgctgt ggagagactt cacctgccac catttccagg tcaacaggac																375
tagagcgttg atgggttttca aaccctgttg gaagaaagtg cccatgggtt ctctgggttct																435
gccartttga cagtttatgg argcttttga atcgtaatar caatgtgagg gtgargtaca																495
cctacagaca ttaaataatt tgctgtgtca aaaaaaaaaa a																536

<210> 286
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..344

<221> sig_peptide
 <222> 90..140
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLITAILAVAVG/FP

<221> polyA_signal
 <222> 500..505

<221> polyA_site
 <222> 515..527

<400> 286																
aatatrarac agctacaata ttccagggcc artcacttgc cattttctcat aacagcgtca																60
gagagaaaaga actgactgar acgttttgag atg aag aaa gtt ctc ctc ctg atc																113
Met Lys Lys Val Leu Leu Leu Ile																
-15 -10																
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag																161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln																
-5 1 5																
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr																209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly																
10 15 20																
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att																257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile																
25 30 35																
cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata																305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile																
40 45 50 55																
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa																354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys																
60 65																
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat																414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta																474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aaacc																529

<210> 287
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..311

<221> sig_peptide
 <222> 57..107
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLITAILAVAVG/FP

<221> polyA_signal
 <222> 467..472

<221> polyA_site
 <222> 482..493

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400> 287
aacttgccat ttctcataac agcgtcagag agaaagaact gactgaaacg tttgag atg      59
                                     Met
aag aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt      107
Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
   -15          -10          -5
ttc cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac      155
Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp
           5          10          15
agc gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca      203
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro
           20          25          30
ttt cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga      251
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg
           35          40          45
cgt aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt      299
Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu
           50          55          60
ccg agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga      351
Pro Ser Glu Lys
65
aattgaaatt gagccacttc cttgargaat caaaattcct gttaataaaa gaaaaacaaa      411
tgtaattgaa atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa      471
acatgaaagc aaaaaaaaaa aa                                          493
  
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<210> 288
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 96..302

<221> sig_peptide

<222> 96..182

<223> Von Heijne matrix

score 5

seq ELSLLPSSLWVLA/TS

<221> polyA_site

<222> 501..514

<400> 288

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aagagacgtc accggctgcg cccttcagta tcgcgacgg aagatggcgt ccgccacccg      60
tctcatccag cggctgcgga actgggctgc cgggc atg acc tgc agg gga agc      113
                               Met Thr Cys Arg Gly Ser
                               -25
tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca      161
Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro
          -20          -15          -10
agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca      209
Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala
          -5          1          5
ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt      257
Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg
10          15          20          25
Crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg      302
Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu
          30          35          40
tagctgccac tgaaraaag gcggtgactc cagctcctcc cataaagagg tgggagctgt      362
cctcggacca gccttacctg tgacactgca ccctcacggc caccgacta ctttgcctcc      422
ttggatttcc tccagggaga atgtgaccta atttatgaca aatacgtara gctcaggtat      482
cacttctagt tttactttaa aaaataaaaa aatagagac      521
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<210> 289

<211> 811

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..526

<221> sig_peptide

<222> 161..328

<223> Von Heijne matrix

score 4.19999980926514

seq XSPLLTALLGQC/SL

<221> polyA_site

<222> 799..811

<400> 289

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aaaaaattgc agtgctgaag aactggacc cgcaaaaggc tgtccctccc aaacctggga      60
ttctgggctc actgagttca cctgcgagtc agccctacct gcactgctct ggtctagtag      120
aacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc      175
```

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Met Val Pro Trp Pro
-55
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc 223
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe
-50 -45 -40
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct 271
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser
-35 -30 -25 -20
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg 319
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu
-15 -10 -5
ggg cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa 367
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln
1 5 10
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg 415
Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp
15 20 25
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaa 463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys
30 35 40 45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt 511
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val
50 55 60
Caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaas ccttcaaara 566
Gln Phe Phe Leu Gly
65
caatgttatt acagcaktct ccccttatcc aaaktttcct tttcctgadt ttcagtttagc 626
tatgggtcaac cgcttggaata atakttgaac acagtacaat aaratatttt gaggtctggga 686
ktggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact 746
tgaaccagg aktttgarac caccctgggc aacatrgtra gacctcatct ctacaaaaaa 806
aaaaa 811

<210> 290
<211> 625
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..332

<221> sig_peptide
<222> 210..299
<223> Von Heijne matrix
score 8.10000038146973
seq ITCLLAFWVPASC/IQ

<221> polyA_signal
<222> 594..599

<221> polyA_site
<222> 613..625

<400> 290
acaggtcsmc ttaacatctc ttgatttgag ccactccac tgtcatcagc tttcacctgg 60

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attatcgtga cagcctccta ctgcttctct atcatgtggc cagagctatc ttccctaaaa 120
atgcattgca tagttgatca agtcactctc tggcctaaaa ccttccttgg ctccctgctg 180
ccctcaggat aaagtctgga cccctcagc atg gct tgt gag act cat ggt gtc 233
                               Met Ala Cys Glu Thr His Gly Val
                               -30 -25
ctt gtc cct gct cac ctg tct ggt ctg atc act tgc ctt ctt gca ttc 281
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe
      -20      -15      -10
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca 329
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro
      -5      1      5      10
ctc tgattcctcc tttcttttgg tcacagagaa aggggtacttt ctctgtcaaa 382
Leu
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgaccccc 442
accctggcat actacacara tcaactctggg ctcaacttggc tgcctaattgg tcactctccc 502
agtaaaactgt aagctccttg agggcaagga ttgtgttgga atttttgtat taacagtggc 562
tggcttggtg cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaa 622
aaa 625

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<210> 291
<211> 684
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 212..361
<221> sig_peptide
<222> 212..319
<223> Von Heijne matrix
      score 4.09999990463257
      seq HWLFLASLSGIKT/YQ
<221> polyA_signal
<222> 650..655
<221> polyA_site
<222> 673..684

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<400> 291
atccccawns cactctctca cagagactgt tcttttcctt ctgagaccct actccagctt 60
gtagttctaa atctgtgatt atgcactgtc tgtcttcctc ttgaggtcag gggccatttc 120
ttttgttctc tgctatgctc aggaccagga tcaaaggagc tcagtaacta tttacaggcg 180
tacatcatat gtggaggaca cttatgctgt g atg gcc cca cac aca gct tcc 232
                               Met Ala Pro His Thr Ala Ser
                               -35 -30
ttt ggg gtc tgt ccc ctg ctg tcc gtt acc cgc gtg gta gcc act gag 280
Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu
      -25      -20      -15
cac tgg ctg ttc ctg gct tca ctg tct ggc atc aaa act tat cag tcc 328
His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser
      -10      -5      1
tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattaccta attcacacra 381
Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile

```



```

5                               10
agggtgtaaat ggtggtaatg gcataktatt tattacccca ggggaccak aacggtggta 441
tcaaaacata tcattcccca gtgggtttaa actctggtag ctttccargg aatccaaagt 501
ggaatccagt ctcccttagct gawttcacag ggccccgtct gcacaacttg gcttctgtcg 561
gcttccttan ccttgacttc ccaagcctta gtcatcaccc tctctccac ccagggtca 621
gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcac yaaaaaaaaa 681
aaa 684
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<210> 292
<211> 628
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 75..482

<221> sig_peptide
<222> 75..128
<223> Von Heijne matrix
score 3.59999990463257
seq KMLISVAMLGAXA/GV

<221> polyA_signal
<222> 595..600

<221> polyA_site
<222> 618..627

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<400> 292
aagtgagacc ggcggaac agcttgccgc tgcggggagc tcccgtgggc gctccgctgg 60
ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
-15 -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg 158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
-5 1 5 10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg 206
Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
15 20 25
cag gac cca agg agc agg gag gag gcg gcc agg acc cag cag cta ttg 254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
30 35 40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg 302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
45 50 55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac 350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His
60 65 70
cgt gag acc gga ctt gcc tcc gtg ggc gcc gga cct tgg ctt ggg cgc 398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
75 80 85 90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg 446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
95 100 105
```

```

amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg      492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
      110                      115
tcgggtgagc acgtgtcccc caaacctgg actgactgct ttaaggtccg caaggcgggc      552
cagggccgag acgcgagtcg gatgtggtga actgaaagaa ccaataaaat catgttcctc      612
cammcaaaaa aaaaaah                                              628

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<210> 293
<211> 813
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 50..631

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<221> sig_peptide
<222> 50..244
<223> Von Heijne matrix
      score 8
      seq LTLIGCLVTGVES/KI

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<221> polyA_signal
<222> 777..782

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<221> polyA_site
<222> 801..812

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<400> 293
aaggaaagga ttactcgagc cttgttagaa tcagacatgg cttcagggg atg cag gac      58
                                   Met Gln Asp
                                   -65
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc      106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser
      -60                      -55                      -50
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg      154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu
      -45                      -40                      -35
cct ttt cag ttc tgt ctc cgg cag gct ttg agg atg aag gct gcg ggc      202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly
      -30                      -25                      -20                      -15
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc      250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile
      -10                      -5                      1
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac      298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp
      5                      10                      15
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat      346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr
      20                      25                      30
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc      394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser
      35                      40                      45                      50
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc      442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg

```

	55		60		65	
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg						490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu						
	70		75		80	
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt						538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val						
	85		90		95	
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt						586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys						
	100		105		110	
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc						631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser						
	115		120		125	
taaactggaa ctggacccag gatgctttgc ascaacgccc taggggtttgc agtgaatgtc						691
caaatgcctg tgtcatcttg tcccgtttcc tcccaatatt ccttctcaaa cttggagagg						751
gaaaattaag ctatactttt aagaaaaataa atatttccat ttaaattgtca amaaaaaaaa						811
ah						813

<210> 294
 <211> 778
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 154..576
 <221> sig_peptide
 <222> 154..360
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MMVLSLGIILASA/SF
 <221> polyA_signal
 <222> 737..742
 <221> polyA_site
 <222> 763..775

<400> 294	
agtaaaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga	60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag	120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc	174
Met Thr Ser Gln Pro Val Pro	
	-65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa	222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln	
	-60
	-55
	-50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa	270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys	
	-45
	-40
	-35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt	318
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys	
	-30
	-25
	-20
	-15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc	366

Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe	
-10 -5 1	
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac	414
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr	
5 10 15	
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg	462
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg	
20 25 30	
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct	510
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa	
35 40 45 50	
gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa	558
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu	
55 60 65	
tct tgt tct cct gtc ggg targataaca ggggttgctt ratttttagat	606
Ser Cys Ser Pro Val Gly	
70	
caattttctta tcagactcaa ataaacattt cttttgaaaa tcatcttatt cttcacatta	666
tcatcttgag ctatgatgga aactagtgas ktctctccag gtttaggcga aaaaaaaatc	726
catgaattag gataaagttg ggaaggaaca ttttatacaa aaaaaaaaah cc	778

<210> 295
 <211> 1060
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 154..897
 <221> sig_peptide
 <222> 154..360
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MMVLSLGIILASA/SF

<221> polyA_signal
 <222> 1017..1022

<221> polyA_site
 <222> 1044..1054

<400> 295	
agtaaaaaaaaa cactggaata aggaagggct gatgactttc agaagatgaa ggtaagtaga	60
aaccgttgat gggactgaga aaccagagtk aaaacctctt tggagcttct gaggactcag	120
ctggaaccaa cgggcacagt tggcaacacc atc atg aca tca caa cct gtt ccc	174
Met Thr Ser Gln Pro Val Pro	
-65	
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa	222
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln	
-60 -55 -50	
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa	270
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys	
-45 -40 -35	
cat cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt	318

His	Leu	His	Ala	Glu	Xaa	Lys	Val	Ile	Gly	Thr	Ile	Gln	Ile	Leu	Cys		
-30					-25					-20					-15		
ggc	atg	atg	gta	ttg	agc	ttg	ggg	atc	att	ttg	gca	tct	gct	tcc	ttc	366	
Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile	Ile	Leu	Ala	Ser	Ala	Ser	Phe		
				-10					-5					1			
tct	cca	aat	ttt	acc	caa	gtg	act	tct	aca	ctg	ttg	aac	tct	gct	tac	414	
Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser	Thr	Leu	Leu	Asn	Ser	Ala	Tyr		
	5					10					15						
cca	ttc	ata	gga	ccc	ttt	ttt	ttt	atc	atc	tct	ggc	tct	cta	tca	atc	462	
Pro	Phe	Ile	Gly	Pro	Phe	Phe	Phe	Ile	Ile	Ser	Gly	Ser	Leu	Ser	Ile		
	20					25					30						
gcc	aca	aaa	aaa	agg	tta	acc	aac	ctt	ttg	gtg	cat	acc	acc	ctg	gtt	510	
Ala	Thr	Lys	Lys	Arg	Leu	Thr	Asn	Leu	Leu	Val	His	Thr	Thr	Leu	Val		
35					40					45					50		
gga	agc	att	ctg	agt	gct	ctg	tct	gcc	ctg	gtg	ggg	ttc	att	ayc	ctg	558	
Gly	Ser	Ile	Leu	Ser	Ala	Leu	Ser	Ala	Leu	Val	Gly	Phe	Ile	Xaa	Leu		
				55					60					65			
tct	gtc	aaa	cag	gcc	acc	tta	aat	cct	gcc	tca	ctg	cak	tgt	gag	ttg	606	
Ser	Val	Lys	Gln	Ala	Thr	Leu	Asn	Pro	Ala	Ser	Leu	Xaa	Cys	Glu	Leu		
			70					75					80				
gmc	aaa	aat	aat	ata	cca	aca	ara	akt	tat	gtt	yct	tac	ttt	tat	cat	654	
Xaa	Lys	Asn	Asn	Ile	Pro	Thr	Xaa	Xaa	Tyr	Val	Xaa	Tyr	Phe	Tyr	His		
		85					90					95					
gat	tca	ctt	tat	acc	acg	gac	kgc	tat	aca	gcc	aaa	gcc	akt	ctg	gct	702	
Asp	Ser	Leu	Tyr	Thr	Thr	Asp	Xaa	Tyr	Thr	Ala	Lys	Ala	Xaa	Leu	Ala		
	100					105				110							
gga	act	ctc	tct	ctg	atg	ctg	att	tgc	act	ctg	ctg	gaa	ttc	tgc	cwa	750	
Gly	Thr	Leu	Ser	Leu	Met	Leu	Ile	Cys	Thr	Leu	Leu	Glu	Phe	Cys	Xaa		
	115				120					125					130		
sct	gtg	ctc	act	gct	gtg	ctg	cgg	tgg	aaa	cag	gct	tac	tct	gac	ttc	798	
Xaa	Val	Leu	Thr	Ala	Val	Leu	Arg	Trp	Lys	Gln	Ala	Tyr	Ser	Asp	Phe		
				135					140					145			
cct	ggg	agt	gta	ctt	ttc	ctg	cct	cam	agt	tac	att	ggw	aat	tct	ggm	846	
Pro	Gly	Ser	Val	Leu	Phe	Leu	Pro	Xaa	Ser	Tyr	Ile	Gly	Asn	Ser	Gly		
			150					155					160				
atg	tcc	tca	aaa	atg	acy	cat	gac	tgt	gga	tat	gaa	gaa	cta	ttg	act	894	
Met	Ser	Ser	Lys	Met	Thr	His	Asp	Cys	Gly	Tyr	Glu	Glu	Leu	Leu	Thr		
		165					170					175					
tct	taagaaaaaa	gggagaaata	ttaatcagaa	agttgattct	tatgataata											947	
Ser																	
tggaagagtt	aaccattata	gaaaagcaaa	gcttgagttt	cctaaatgta	agctttttaa											1007	
gtaatgaaca	ttaaaaaaaaa	ccattatttc	actgtcaaaa	aaaaaaamcc	nkt											1060	

<210> 296

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 146..292

<221> sig_peptide

<222> 146..253

<223> Von Heijne matrix

score 5.5
seq FTSMCILFHCLLS/FQ

<221> polyA_signal
<222> 395..400

<221> polyA_site
<222> 433..444

<400> 296
aacttgggac aagaratcaa acttttaaaga tgggtctaaag cccctcttaa aggtctgact 60
gtgtcggacc tctagagcta atctcactag atgtgagcca ttgtttatat tctagccatc 120
ctttcatttc attctagaag acccc atg caa gtt ccc cac cta agg gtc tgg 172
Met Gln Val Pro His Leu Arg Val Trp
-35 -30
aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca 220
Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
-25 -20 -15
agt atg tgc ata ttg ttc cac tgt ctt ctt agc ttt cag gtt ttc aaa 268
Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
-10 -5 1 5
aag aaa aga aaa ctt ara ctt ttc tgatgttctt ttttacgtaa ataaccattt 322
Lys Lys Arg Lys Leu Xaa Leu Phe
10
tattgttggtt ttgctttttc tgccttcaaa ctactcccac aggccaaata tavctggctg 382
cttctttctg taaataaagt tttattgggc cacagccatg gccatctttt aaaaaaaaaa 442
aa 444

<210> 297
<211> 754
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 126..383

<221> sig_peptide
<222> 126..167
<223> Von Heijne matrix
score 7.5
seq VALNLILVPCCAA/WC

<221> polyA_signal
<222> 726..731

<221> polyA_site
<222> 743..754

<400> 297
aattgtatgt tacgatgttg tattgatttt taagaaagta attkratttg taaaactttct 60
gctcgtttac actgcacatt gaatacaggt aactaattgg wwggagaggg gaggtcactc 120
ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg 170
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp
-10 -5 1

tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct	218
Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser	
5 10 15	
gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt	266
Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly	
20 25 30	
tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga	314
Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg	
35 40 45	
ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag	362
Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu	
50 55 60 65	
gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar	413
Gly His Arg Ile Cys Asp Leu	
70	
aaaccacagt cttcccagca attattacaa ttcttgaatt ccttggggat tttttactgc	473
cctttcaaag cacttaaktg tkrratctaa cgtkttccag tgtctgtctg aggtgactta	533
aaaaatcaga acaaaacttc tattatccag agtcatggga gagtacaccc tttccaggaa	593
taatgttttg ggaaacactg aaatgaaatc ttcccagtat tataaattgt gtatttataa	653
aaaagaaact tttctgaatg cctacctggc ggtgtatacc aggcagtgtg ccagtttaaa	713
aagatgaaaa agaataaaaa cttttgagga aaaaaaaaaa a	754

<210> 298
 <211> 629
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 66..497
 <221> sig_peptide
 <222> 66..239
 <223> Von Heijne matrix
 score 5.40000009536743
 seq QLLDSVLWL GALG/LT

<221> polyA_signal
 <222> 594..599

<221> polyA_site
 <222> 618..629

<400> 298	
aactcccaga atgctgacca aagtgggagg agcactaggt cttcccgatca cctccacctc	60
tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg	110
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro	
-55 -50 -45	
atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt	158
Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser	
-40 -35 -30	
cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc	206
Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu	
-25 -20 -15	
ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca	254

Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala	
-10 -5 1 5	
gtc ttt tcc acc act ggc cca gcc ctg ctg ctg ctt ctg gtc agc ttc	302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe	
10 15 20	
ctc acc ttt gac ctg ctc cat agg ccc gca gtc aca ctc tgc cac agc	350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser	
25 30 35	
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg	398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu	
40 45 50	
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac	446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn	
55 60 65	
tta gcc tcc agg aag cac tgc tgc tgc tgc tca tgg ggc tgg gcc cgc	494
Leu Ala Ser Arg Lys His Cys Cys Cys Cys Ser Trp Gly Trp Ala Arg	
70 75 80 85	
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct	547
Ser	
ccatccttggt gctgagakanc ccctccccac aactcagtgt ccttcaaata tacaatgacc	607
acccttcttc aaaaaaaaaa aa	629

<210> 299
 <211> 765
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 49..411
 <221> sig_peptide
 <222> 49..96
 <223> Von Heijne matrix
 score 10.1000003814697
 seq LVLTLCTLPLAVA/SA

<221> polyA_signal
 <222> 732..737

<221> polyA_site
 <222> 750..763

<400> 299	
aaagatccct gcagccccggc aggagagaag gctgagcctt ctggcgctc atg gag agg	57
Met Glu Arg	
-15	
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc	105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly	
-10 -5 1	
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag	153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys	
5 10 15	
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac	201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp	

20	25	30	35	
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc				249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro				
	40	45	50	
ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg				297
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro				
	55	60	65	
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc				345
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly				
	70	75	80	
cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tcg				393
Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser				
	85	90	95	
ggc gag cat ccs rva btg tgaatkkkga cttttttctc ckccatttga				441
Gly Glu His Pro Xaa Xaa				
100	105			
agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tcaactgaatt tacaaaraca				501
gcaggaacrs ackggtgggg atgggcagct gttcragcr atggggtkac tgcccttcct				561
ggcacagcac artacacctg ccatacaacc carcatcagg cakgctgcac tggaatcgat				621
acagtgtatg acaatgtcat atagtataac acaacataat gaatataacg tgtatattgc				681
aacttaatat aatacgaatg aatataatgc tacataatac aacataatat aataaaaatag				741
aatgcaacac aaaaaaaaaa aacc				765

<210> 300

<211> 623

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 49..534

<221> sig_peptide

<222> 49..96

<223> Von Heijne matrix

score 10.1000003814697

seq LVLTLCTLPLAVA/SA

<221> polyA_signal

<222> 593..598

<221> polyA_site

<222> 612..623

<400> 300

aaagatccct gcagcccggc aggagagaag gctgagcctt ctggcgtc atg gag agg	57
	Met Glu Arg
	-15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc	105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly	
	-10
	-5
	1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag	153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys	
	5
	10
	15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac	201

Val	Ser	Ser	Trp	Thr	Glu	Cys	Pro	Pro	Thr	Trp	Cys	Ser	Pro	Leu	Asp	
20					25					30					35	
caa	gtc	tgc	atc	tcc	aac	gag	gtg	gtc	gtc	tct	ttt	aaa	tgg	agt	gta	249
Gln	Val	Cys	Ile	Ser	Asn	Glu	Val	Val	Val	Ser	Phe	Lys	Trp	Ser	Val	
				40					45					50		
cgc	gtc	ctg	ctc	agc	aaa	cgc	tgt	gct	ccc	aga	tgt	ccc	aac	gac	aac	297
Arg	Val	Leu	Leu	Ser	Lys	Arg	Cys	Ala	Pro	Arg	Cys	Pro	Asn	Asp	Asn	
				55				60					65			
atg	aak	ttc	gaa	tgg	tcg	ccg	gcc	ccc	atg	gtg	caa	ggc	gtg	atc	acc	345
Met	Xaa	Phe	Glu	Trp	Ser	Pro	Ala	Pro	Met	Val	Gln	Gly	Val	Ile	Thr	
				70			75					80				
agg	cgc	tgc	tgt	tcc	tgg	gct	ctc	tgc	aac	agg	gca	ctg	acc	cca	cag	393
Arg	Arg	Cys	Cys	Ser	Trp	Ala	Leu	Cys	Asn	Arg	Ala	Leu	Thr	Pro	Gln	
				85			90				95					
gag	ggg	cgc	tgg	gcc	ctg	cra	ggg	ggg	ctc	ctg	ctc	cag	gac	cct	tcg	441
Glu	Gly	Arg	Trp	Ala	Leu	Xaa	Gly	Gly	Leu	Leu	Leu	Gln	Asp	Pro	Ser	
100					105				110						115	
agg	ggc	ara	aaa	acc	tgg	gtg	cgg	cca	cag	ctg	ggg	ctc	cca	ctc	tgc	489
Arg	Gly	Xaa	Lys	Thr	Trp	Val	Arg	Pro	Gln	Leu	Gly	Leu	Pro	Leu	Cys	
				120				125					130			
ctt	ccc	awt	tcc	aac	ccc	ctc	tgc	cca	rgg	gaa	acc	cag	gaa	gga		534
Leu	Pro	Xaa	Ser	Asn	Pro	Leu	Cys	Pro	Xaa	Glu	Thr	Gln	Glu	Gly		
				135			140					145				
taacactgtg	ggtgccccca	cctgtgcatt	gggaccacra	cttcaccctc	ttggaracaa											594
taaaactctca	tgcccccaaaa	aaaaaaaaaa														623

<210> 301

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 86..415

<221> sig_peptide

<222> 86..145

<223> Von Heijne matrix

score 9.80000019073486

seq FTIGLTLGLGXQA/MP

<221> polyA_signal

<222> 540..545

<221> polyA_site

<222> 560..571

<400> 301

aaaaactcac ccagtgagtg tgagcattta agaagcatcc tctgccaaga ccaaaaggaa 60

agaagaaaaaa bggccaaaaag ccaaaa atg ara ctg atg gta ctt gtt ttc acc 112

Met Xaa Leu Met Val Leu Val Phe Thr

-20 -15

att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc 160

Ile Gly Leu Thr Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg

-10

-5

1

5

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ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt      208
Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu
      10                      15                      20
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat      256
Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp
      25                      30                      35
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc      304
His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe
      40                      45                      50
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat      352
Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp
      55                      60                      65
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct      400
Leu Phe Arg Asp Ser Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser
      70                      75                      80                      85
ggc gaa cac cat tcc tgatttccca caaactgcac tacatcagta taactgcatt      455
Gly Glu His His Ser
      90
tctagttttct atatagtgc atagagcata gattctataa attcttactt gtctaagaaa      515
gtaaatctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaa      571

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<210> 302
<211> 612
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 56..268
<221> sig_peptide
<222> 56..100
<223> Von Heijne matrix
score 4.59999990463257
seq LLTHNLLSSHVRG/VG

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<221> polyA_signal
<222> 584..589

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<221> polyA_site
<222> 601..612

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<400> 302
ctaatacgaaa aggggggattt tccgggttccg gcctggcgag agtttggtgcg gcgac atg      58
                                         Met
                                         -15
aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg      106
Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly
      -10                      -5                      1
tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc      154
Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys
      5                      10                      15
cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg      202
Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val
      20                      25                      30

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gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag      250
Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln
35              40              45              50
gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagtttct      298
Val Pro Arg Arg Ala Gly
55
gaggaccatg caccacctgc tgctggaggt ggamstgaka gagggcaccc tgcagtgtccc      358
ggaatctgga cgtatgttcc ccatcagccg cgggatcccc aacatgctgc tgagtgaaga      418
ggaaactgag agttgattgt gccaggcgcc agtttttctt gttatgactg tgtatttttg      478
ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac      538
accaaacaca gtgtttttga gctcgggtatt atatattttt ttctcattaa aggtttaaaa      598
ccaaaaaaaa aaaa      612

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<210> 303
<211> 539
<212> DNA
<213> Homo sapiens

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<220>

<221> CDS

<222> 32..328

<221> sig_peptide

<222> 32..103

<223> Von Heijne matrix

score 4.59999990463257

seq FFIFCSLNTLLLG/GV

<221> polyA_signal

<222> 508..513

<221> polyA_site

<222> 528..539

<400> 303

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aaacaactatc ctgcctgctg cttgctgcac c atg aag tct gcc aag ctg gga      52
Met Lys Ser Ala Lys Leu Gly
-20
ttt ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg      100
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu
-15 -10 -5
ggt ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat      148
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp
1 5 10 15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt      196
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe
20 25 30
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc      244
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe
35 40 45
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt      292
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg
50 55 60
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg      338
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg

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65	70	75	
tgaactcatg	aagttgtctg	ctgcaccatc	cgaaataaag acacaagaaa attcaractg 398
atttwgaaat	ctttgttwta	tttccmymak	ggcgwhtaag cttccatatg tttgctatgt 458
tcctgaccct	agttttgtct	ttcctggaaa	ttaactgtat gakkattasa atgaaagagt 518
ctttctgtca	aaaaaaaaaa	a	539

<210> 304
 <211> 964
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..527

<221> sig_peptide
 <222> 21..95
 <223> Von Heijne matrix
 score 8.5
 seq LKVLPLAPAAA/QD

<221> polyA_signal
 <222> 921..926

<221> polyA_site
 <222> 953..963

<400> 304
 agggcgatc ttctccggcc atg agg aag cca gcc gct ggc ttc ctt ccc tca 53
 Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser
 -25 -20 -15
 ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat 101
 Leu Leu Lys Val Leu Leu Pro Leu Ala Pro Ala Ala Gln Asp
 -10 -5 1
 acg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac 149
 Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr
 5 10 15
 caa cgc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc 197
 Gln Arg Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr
 20 25 30
 tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag 245
 Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln
 35 40 45 50
 ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc 293
 Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys
 55 60 65
 tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act 341
 Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr
 70 75 80
 cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt 389
 His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys
 85 90 95
 tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa 437
 Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu
 100 105 110

sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc	485
Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr	
115 120 125 130	
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc	527
Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala	
135 140	
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgctccc tgggaggcca	587
ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca	647
agaacacaag caggaagagg ggcagaaaaca ggaagagcaa gaagaggaac aggaagagga	707
gggaaagcag gaagaaggac aggggactaa ggagggacgg gaggctgtgt ctcagctgca	767
gacagactca gagcccaagt ttcactctga atctctatct tctaaccctt cctcttttgc	827
tccccgggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat	887
tcgatcagcc caggaaatag atgaaatgaa tgaaatatat gatgagaact cctactggag	947
aaacccaaaaa aaaaaak	964

<210> 305

<211> 684

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 147..647

<221> sig_peptide

<222> 147..374

<223> Von Heijne matrix

score 3.5

seq LASASELPLGSRP/AP

<221> polyA_site

<222> 668..681

<400> 305

aaacttcctgt gagcccggcg gtgacaacgg caacatggcc cgtgaacgga gctgaagtcg	60
acgacttctc ctrgrarmcc ccgactgagg cggagacgaa ggtgctgcag gcgcgacggg	120
agcggcaaga tcgcatctcc cggctc atg ggc gac tat ctg ctg cgc ggt tac	173
Met Gly Asp Tyr Leu Leu Arg Gly Tyr	
-75 -70	
cgc atg ctg ggc gag acg tgt gcg gac tgc ggg acg atc ctc ctc caa	221
Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln	
-65 -60 -55	
gac aaa cag cgg aaa atc tac tgc gtg gct tgt cag gaa ctc gac tca	269
Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser	
-50 -45 -40	
gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc	317
Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser	
-35 -30 -25 -20	
caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc	365
Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly	
-15 -10 -5	
tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag	413
Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu	
1 5 10	
gga gct gca gca gga ctc aag gca gcc cag ggg cca cct gct cct gct	461

Gly	Ala	Ala	Ala	Gly	Leu	Lys	Ala	Ala	Gln	Gly	Pro	Pro	Ala	Pro	Ala		
15						20				25							
gtg	cct	cca	aat	aca	rat	gtc	atg	gcc	tgc	aca	cag	aca	gcc	ctc	ttg	509	
Val	Pro	Pro	Asn	Thr	Xaa	Val	Met	Ala	Cys	Thr	Gln	Thr	Ala	Leu	Leu		
30					35				40					45			
caa	aag	ctg	acc	tgg	gcc	tct	gct	gaa	ctg	ggc	tct	anc	acc	tcc	cyg	557	
Gln	Lys	Leu	Thr	Trp	Ala	Ser	Ala	Glu	Leu	Gly	Ser	Xaa	Thr	Ser	Xaa		
			50			55				60							
gga	aaa	mta	gca	tcc	agc	tgt	gtg	gcc	tta	tcc	gcg	cat	gtg	cgg	agg	605	
Gly	Lys	Xaa	Ala	Ser	Ser	Cys	Val	Ala	Leu	Ser	Ala	His	Val	Arg	Arg		
			65			70				75							
ccc	tgc	gca	gcc	tgc	agc	agc	tac	agc	act	aag	aga	agc	ccc			647	
Pro	Cys	Ala	Ala	Cys	Ser	Ser	Tyr	Ser	Thr	Lys	Arg	Ser	Pro				
	80					85				90							
tgagaaaaac	ctctagaaaa	acaaaaaaaa	aaaaccc													684	

<210> 306

<211> 693

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 262..471

<221> sig_peptide

<222> 262..306

<223> Von Heijne matrix

score 3.5

seq LCFLLPHHRLQEA/RQ

<221> polyA_signal

<222> 663..668

<221> polyA_site

<222> 682..693

<400> 306

atttcgcggc	gctcgcgbma	cyhsgwtgtt	cagcaccttc	ggctccggttg	aggttgtcaa	60	
gtcggmccaa	acagggttg	tctctgcagt	ttccaacatg	gcagggmsgt	ttaatagaca	120	
tggataagaa	gtccactcac	agaaatcctg	aagatgccag	ggctggcaaa	tatgaaggta	180	
aacacaaaacg	aaagaaaaga	agaaagcaaa	accaaaacca	gcaccgatcc	cgacatagat	240	
cagtgcgctc	tttttcttca	g atg atc cta	tgt ttc ctt	ctt cct cat	cat	291	
		Met Ile Leu Cys Phe	Leu Leu Pro His His				
		-15	-10				
cgt ctt cag	gaa gcc aga	cag att caa	gta ttg aag	atg ctt cca	agg	339	
Arg Leu Gln	Glu Ala Arg	Gln Ile Gln	Val Leu Lys	Met Leu Pro	Arg		
-5	1	5	10				
gaa aaa tta	aga aga aga	gaa gag aga	aaa caa ata	aat ggg aaa	aaa	387	
Glu Lys Leu	Arg Arg Arg	Glu Glu Arg	Lys Gln Ile	Asn Gly Lys	Lys		
	15	20	25				
raa agg aca	aaa tat gaa	aca cca aga	aaa rga raa	gga aaa aaa	gga	435	
Xaa Arg Thr	Lys Tyr Glu	Thr Pro Arg	Lys Xaa Xaa	Gly Lys Lys	Gly		
	30	35	40				
gga aac mac	cmc wtw tkt	cmc ctt tcc	aar agg gac	tgaaactggg		481	

Gly	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Ser	Lys	Arg	Asp	
45						50				55		
ctgacccttt	tgatttccaa	vctcascgtt	ttggtgtaag	gcggccaaar	aaggatgcgg							541
ascccagcac	tgtgaagcct	acaaaaacat	tgatgcgctg	gcttggggat	ttgaatttga							601
acatctttca	cactaagttc	agactcatga	aaccaatctt	cagatgctct	gtaaaccaca							661
taataaagag	tttggaatt	aaaaaaaaar	aa									693

<210> 307
<211> 1656
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..1216

<221> sig_peptide
<222> 74..172
<223> Von Heijne matrix
score 5.80000019073486
seq XLCLGMALCPRQA/TR

<221> polyA_signal
<222> 1627..1632

<221> polyA_site
<222> 1640..1652

<400> 307	
atctcttggc gtctcaacgt tcggatcagc agcttttttc cattctctct ctccacttct	60
tcagtgcagca gcc atg agt tgg act gtg cct gtt gtg cgg gcc agc cag	109
Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln	
-30 -25	
aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg	157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu	
-20 -15 -10	
tgt ccg cgt caa gca acg cgc atc ccg ctc aac ggc acc tgg ctc ttc	205
Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe	
-5 1 5 10	
acc ccc gtg agc aag atg gcg act gtg aar agt gag ctt att gag cgt	253
Thr Pro Val Ser Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg	
15 20 25	
ttc act tcc gar aag ccc gtt cat cac agt aag gtc tcc atc ata gga	301
Phe Thr Ser Glu Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly	
30 35 40	
act gga tcg gtg ggc atg gcc tgc gct atc agc atc tta tta aaa ggc	349
Thr Gly Ser Val Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly	
45 50 55	
ttg agt gat gaa ctt gcc ctt gtg gat ctt gat gaa rac aaa ctg aag	397
Leu Ser Asp Glu Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys	
60 65 70 75	
ggg gag acr atg gat ctt caa cat ggc agc cct ttc acg aaa atg cca	445
Gly Glu Thr Met Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro	
80 85 90	
aat att gtt tgt agc aaa rat tac ttt gtc aca gca aac tcc aac cta	493

Asn Ile Val Cys Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu	
95 100 105	
gtg att atc aca gca ggt gca cgc caa raa aag gga gaa acg cgc ctt	541
Val Ile Ile Thr Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu	
110 115 120	
aat tta stc cag cga aat gtg gcc atc ttc aag tta atg att tcc agt	589
Asn Leu Xaa Gln Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser	
125 130 135	
att gtc cag tac agc ccc cac tgc aaa ctg att att gtt tcc aat cca	637
Ile Val Gln Tyr Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro	
140 145 150 155	
gtg gat atc tta act tat gta gct tgg aag ttg agt gca ttt ccc aaa	685
Val Asp Ile Leu Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys	
160 165 170	
aac cgt att att gga agc ggc tgt aat ctg ata mhg gct cgt ttt cgt	733
Asn Arg Ile Ile Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg	
175 180 185	
ttc ttg att gga caa aag ctt ggt atc cat tct gaa agc tgc cat gga	781
Phe Leu Ile Gly Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly	
190 195 200	
tgg atc ctc gga gag cat gga gac tca agt gtt cct gtg tgg agt gga	829
Trp Ile Leu Gly Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly	
205 210 215	
gtg aac ata gct ggt gtc cct ttg aag gat ctg aac tct gat ata gga	877
Val Asn Ile Ala Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly	
220 225 230 235	
act gat aaa gat cct gag caa tgg aaa aat gtc cac aaa gaa gtg act	925
Thr Asp Lys Asp Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr	
240 245 250	
gca act gcc tat gag att att aaa atg aaa ggt tat act tct tgg gcc	973
Ala Thr Ala Tyr Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala	
255 260 265	
att ggc cta tct gtg gcc gat tta aca gaa agt att ttg aag aat ctt	1021
Ile Gly Leu Ser Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu	
270 275 280	
agg aga ata cat cca gtt tcc acc ata act aag ggc ctc tat gga ata	1069
Arg Arg Ile His Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile	
285 290 295	
rat gaa gaa gta ttc ctc agt att cct tgt atc ctg gga gag aac ggt	1117
Xaa Glu Glu Val Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly	
300 305 310 315	
att acc aac ctt ata aag ata aag ctg acc cct gaa gaa gag gcc cat	1165
Ile Thr Asn Leu Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His	
320 325 330	
ctg aaa aaa agt gca aaa aca ctc tgg gaa att cag aat aag ctt aag	1213
Leu Lys Lys Ser Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys	
335 340 345	
ctt taaagttgcc taaaactacc attccgaaat tattgaagag atcatagata	1266
Leu	
caggattata taacgaaatt ttgaataaac ttgaattcct aaaagatgga aacaggaaaag	1326
taggtagagt gatttttcccta tttattttagt cctccagctc ttttattgag catccacgtg	1386
ctggacgata cttattttaca attcckaagt atttttggtta cctctgatgt agcagcactt	1446
gccatgttat atatatgtag ttgrmatttg gttcccaaaa agtaggatgt aggtatttat	1506
tgtgttctag aaattccgac tctttttcatt agatatatgc tatttctttc attcttgctg	1566
gtttatacct atgttcattt atatgctgta aaaaagtagt agcttcttct acaatgtaaa	1626
aataaatgta catacaaaaa aaaaaamcmc	1656

<210> 308
 <211> 517
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..164

<221> sig_peptide
 <222> 48..89
 <223> Von Heijne matrix
 score 4
 seq YYMVCLFFRLIFS/EH

<221> polyA_signal
 <222> 482..487

<221> polyA_site

<222> 505..517

<400> 308

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aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac      56
                                     Met Tyr Tyr
atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att      104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile
   -10          -5          1          5
ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca      152
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro
           10          15          20
aca tct gct ggc taaataaaga catgatcttc accttttggg attgttaatt      204
Thr Ser Ala Gly
           25
taaaaatgggtt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctggtg      264
attttatatgg ctcttcacaa ggtgttatatt tggggatatca aggtatggat gcttaaatca      324
gctgcaggaa gtaagaaaga agaaaaaagg agtgataaag ataaaaaaaa atcaaccttg      384
gtccttccac caaaaacccat taatttccat atcatcatct gcataararg gaaaattcct      444
acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg      504
aaaaaaaaaa aaa                                          517
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<210> 309
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 185..334

<221> sig_peptide
 <222> 185..295
 <223> Von Heijne matrix
 score 5.90000009536743

seq LSYASSALSPCLT/AP

<221> polyA_signal

<222> 355..360

<221> polyA_site

<222> 392..405

<400> 309

atcaccttct tctccatcct tstctgggcc agtccccarc ccagtcacctc tcctgacctg 60

cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct 120

ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg 180

tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg 229

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val

-35 -30 -25

aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc 277

Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala

-20 -15 -10

ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg 325

Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met

-5 1 5 10

cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc 374

Pro Asp Asn

cccaraagggt tttctaaaaa caaaaaaaaaa a 405

<210> 310

<211> 1087

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 195..347

<221> sig_peptide

<222> 195..272

<223> Von Heijne matrix

score 7.09999990463257

seq LASLQWSLTAWC/GS

<221> polyA_signal

<222> 1037..1042

<221> polyA_site

<222> 1071..1082

<400> 310

aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt 60

acctacctta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg 120

gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgaccc agttgctggc 180

ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg 230

Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg

-25 -20 -15

cct ctc gct tct ttg cag tgg agc ctg aca ctg gcg tgg tgt ggc tcc 278

Pro Leu Ala Ser Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser

	-10	-5	1	
ggc agc cac tgg aca gag aga cca akt cag akt tca ccg tgg akt tct				326
Gly Ser His Trp Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser				
	5	10	15	
ctg tca gcg acc acc agg ggg tgatcacacg gaaggtgaac atccaggtcg				377
Leu Ser Ala Thr Thr Arg Gly				
	20	25		
gggatgtgaa tgacaacgcg cccacatttc acaatcagcc ctacagcgtc cgcattccctg				437
araatacacc agtgggggacg cccatcttca tcgtgaatgc cacagacccc gacttggggg				497
cagggggcag cgtcctctac tccttccagc cccctccca attcttcgcc attgacagcg				557
cccgcggtat cktcacagt atccgggagc tggactacga taccacrcmg gcctaccagc				617
tcwcggtcwa cgccacagat caagacaara ccaggcctct gtccaccstg gccaaacttg				677
ccatcatcat cacagatgtc caggacatgg accccatctt catcaacctg ccttacagca				737
ccaacatcta cgagcattct cctccgggca cgacggtgcg catcatcacc gccatagacc				797
aggataaaagg acgtccccgg ggcattggct acaccatcgt ttcagggcat ctgtgtttac				857
aagaacccaa gatctctcag gagctcagga aaaggggctt gctgtgaggc tcagggttcc				917
catggacatt ctgagctgac cctcctcagc attggatctc ctggctcagg aactaggaac				977
gaagcttga tggtttctcc tttcctacag catctgtatt catttcctat agttgccata				1037
ataaaatgcc actaaacttag tggcttaaaa accaaaaaaa aaaaaccctt				1087

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<210> 311
<211> 916
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..815

<221> sig_peptide
<222> 90..179
<223> Von Heijne matrix
      score 13.1999998092651
      seq LLLLSTLVIPSAA/AP

<221> polyA_signal
<222> 883..888

<221> polyA_site
<222> 905..916

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<400> 311	
aaaacagtac gtgggcggcc ggaatccggg agtccggtga cccgggctgt ggtctagcat	60
aaaggcggag ccagaagaag gggcggggt atg gga gaa gcc tcc cca cct gcc	113
Met Gly Glu Ala Ser Pro Pro Ala	
-30 -25	
ccc gca agg cgg cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg	161
Pro Ala Arg Arg His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu	
-20 -15 -10	
gtg atc ccc tcc gct gca gct cct atc cat gat gct gac gcc caa gag	209
Val Ile Pro Ser Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu	
-5 1 5 10	
agc tcc ttg ggt ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc	257
Ser Ser Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser	
15 20 25	

cga ctt ttc ctg aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc	305
Arg Leu Phe Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe	
30 35 40	
tct gcc ccc atg gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag	353
Ser Ala Pro Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu	
45 50 55	
gag aac cag gag cac cag ctg ggg aac aac acc ctc tcc agc cac ctc	401
Glu Asn Gln Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu	
60 65 70	
cag atc gac aag atg acc gac aac aag aca gga gag gtg ctg atc tcc	449
Gln Ile Asp Lys Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser	
75 80 85 90	
gag aat gtg gtg gca tcc att caa cca vcg gag ggg anc ttc gag ggt	497
Glu Asn Val Val Ala Ser Ile Gln Pro Xaa Glu Gly Xaa Phe Glu Gly	
95 100 105	
gat ttg aag gth ccc agg atg gag gar aag gag gcc ctg gta ccc mtc	545
Asp Leu Lys Val Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Xaa	
110 115 120	
car aag gcc acg gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc	593
Gln Lys Ala Thr Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala	
125 130 135	
ttc tgg atc att aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg	641
Phe Trp Ile Ile Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu	
140 145 150	
gag ggc ggc cac tgg ctc anc gar aag cga cac cgc ctg cag gcc atc	689
Glu Gly Gly His Trp Leu Xaa Glu Lys Arg His Arg Leu Gln Ala Ile	
155 160 165 170	
cgg gat gga ctc cgc aag ggg acc cac aag gac rtc cta daa rag ggg	737
Arg Asp Gly Leu Arg Lys Gly Thr His Lys Asp Xaa Leu Xaa Xaa Gly	
175 180 185	
acc gar agc tcc tcc cac tcc agg ctg tcc ccc cga aar amm cac tta	785
Thr Glu Ser Ser Ser His Ser Arg Leu Ser Pro Arg Lys Xaa His Leu	
190 195 200	
ctg tac atc ctc arg ccc tct cgg cag ctg targgggtggg gaccggggar	835
Leu Tyr Ile Leu Xaa Pro Ser Arg Gln Leu	
205 210	
macctgcctg tagcccccat caraccctgc cccaagcacc atatggaaat aaagttcttt	895
cttacatcca aaaaaaaaaa a	916

<210> 312

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..513

<221> sig_peptide

<222> 52..231

<223> Von Heijne matrix

score 4

seq LVRRTLLVAALRA/WM

<221> polyA_signal

<222> 553..558

<221> polyA_site

<222> 572..583

<400> 312

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aaggaaacag caaccagagg gagatgatca cctgaaccac tgctccaaac c atg ggc      57
                                     Met Gly
                                     -60
agt aaa tgc tgt aaa ggt ggt cca gat gaa gat gca gta gaa aga cag      105
Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu Arg Gln
      -55                                -50                                -45
agg cgg cag aag ttg ctt ctt gca caa ctg cat cac aga aaa agg gtg      153
Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys Arg Val
      -40                                -35                                -30
aar gca gct ggg cag atc cag gcc tgg tgg cgt ggg gtc ctg gtg cgc      201
Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu Val Arg
      -25                                -20                                -15
agg acc ctg ctg gtt gct gcc ctc agg gcc tgg atg att cag tgc tgg      249
Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln Cys Trp
      -10                                -5                                1                                5
tgg agg acg ttg gtg cag aga cgg atc cgt cag cgg cgg cag gcc ctg      297
Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln Ala Leu
      10                                15                                20
atc ggg gtc tac gtc atc cag gag cag gcg gcg gtc aag ctc cag tcc      345
Leu Gly Val Tyr Val Ile Gln Glu Gln Ala Ala Val Lys Leu Gln Ser
      25                                30                                35
tgc atc cgc atg tgg cag tgc cgg caa tgt tac cgc caa atg tgc aat      393
Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met Cys Asn
      40                                45                                50
gct ctc tgc ttg ttc cag gtc cca aaa agc agc ctt gcc ttc caa act      441
Ala Leu Cys Leu Phe Gln Val Pro Lys Ser Ser Leu Ala Phe Gln Thr
      55                                60                                65                                70
gat ggc ttt tta cag gtc caa tat gca atc cct tca aag cag cca gag      489
Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln Pro Glu
      75                                80                                85
ttc cac att gaa atc cta tca atc tgaaaggcct ggggcatgga gaacaggctg      543
Phe His Ile Glu Ile Leu Ser Ile
      90
cactacccta ataaatgtct gaccaggtaa aaaaaaaaaa      583

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<210> 313

<211> 697

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 172..438

<221> sig_peptide

<222> 172..354

<223> Von Heijne matrix

score 4.69999980926514

seq LLPCNLHCSWLHS/SP

<221> polyA_signal
<222> 682..687

<221> polyA_site
<222> 685..697

<400> 313
agattggctg ggcagatggg ctgactggct gggcagatgg gtgggtgagt tccctctccc 60
cagagccatc ggccaggtac caaagctcag ctgtatggat tcccaacagg aggacctgcg 120
cttcctggg acccattggt gtactggatt aacaagcgac ggcgctacgg c atg aat 177
Met Asn
-60
gca gcc atc aac acg ggc cct gcc cct gct gtc acc aag act gag act 225
Ala Ala Ile Asn Thr Gly Pro Ala Pro Ala Val Thr Lys Thr Glu Thr
-55 -50 -45
gag gtc cag aat cca gat gtt ctg tgg gat ttg gac atc ccc gaa gcc 273
Glu Val Gln Asn Pro Asp Val Leu Trp Asp Leu Asp Ile Pro Glu Ala
-40 -35 -30
agg agc cat gct gac caa gac agc aac ccc aag gcg gaa gcc ctg ctc 321
Arg Ser His Ala Asp Gln Asp Ser Asn Pro Lys Ala Glu Ala Leu Leu
-25 -20 -15
ccc tgc aac ctg cac tgc agc tgg ctc cac agc agc ccc agg cca gat 369
Pro Cys Asn Leu His Cys Ser Trp Leu His Ser Ser Pro Arg Pro Asp
-10 -5 1 5
ccc cat tcc cac ttc cca tct ktc agg agg tgc cct ttg ccc cac cct 417
Pro His Ser His Phe Pro Ser Xaa Arg Arg Cys Pro Leu Pro His Pro
10 15 20
tgt gca acc tac ccc ccs kgc tgaaccactc tgtctcctat cctttggcca 468
Cys Ala Thr Tyr Pro Pro Xaa
25
cctgtcctga aaggaatggt ctcttccatt cctcctgaa tctggcccag gaagaccata 528
gcttcaatgy caagcctttt ccttcaaaac tgtagcctcc tctcactgaa ggtgggagct 588
gcaggaatca ggtgcagagt aggaaatgga actaacctca ggaaggtggt attgacagag 648
gtcaggaccc acctggatgt catgctatga aacattaaaa gaaaaaaaaa 697

<210> 314
<211> 803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..366

<221> sig_peptide
<222> 148..225
<223> Von Heijne matrix
score 5.5
seq LFTLLFLIMLVLK/LD

<221> polyA_signal
<222> 770..775

<221> polyA_site

<222> 792..803

<400> 314

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aaatggggggg aaaagggcgg aaaaggacaa ggatccaaac tggcgaattt gctgatcttc      60
gcgccctctt ccgctttccg gccggcagcg ctgccagggt atatttcctt ttttccgatac      120
ctgcaacagc ctcttttaaac tgttttaa atg aga atg tcc ttg gct cag aga gta      174
                               Met Arg Met Ser Leu Ala Gln Arg Val
                               -25                               -20

cta ctc acc tgg ctt ttc aca cta ctc ttc ttg atc atg ttg gtg ttg      222
Leu Leu Thr Trp Leu Phe Thr Leu Leu Phe Leu Ile Met Leu Val Leu
                               -15                               -10                               -5

aaa ctg gat gag aaa gca cct tgg aac tgg ttc ctc ata ttc att cca      270
Lys Leu Asp Glu Lys Ala Pro Trp Asn Trp Phe Leu Ile Phe Ile Pro
                               1                               5                               10                               15

gtc tgg ata ttt gat act atc ctt ctt gtc ctg ctg att gtg aaa atg      318
Val Trp Ile Phe Asp Thr Ile Leu Leu Val Leu Leu Ile Val Lys Met
                               20                               25                               30

gct ggg cgg tgt aag tct ggc ttt gac ctc gac atg gat cac aca ata      366
Ala Gly Arg Cys Lys Ser Gly Phe Asp Leu Asp Met Asp His Thr Ile
                               35                               40                               45

taaaaaaaaa aacctggtac ctcatcgtac tgtkacttaa attasccttc tgcctcgcac      426
tctgtgctaa actggaacag tttactacca tgaatctatc ctatgtcttc attcctttat      486
gggccttgct ggctggggct ttaacagaac tcggatataa tgtctttttt gtgaaagact      546
gacttctaag tacatcatct cctttctatt gctgttcaac aagttaccat taaagtgttc      606
tgaatctgtc aagcttcaag aataccagag aactgaggga aaataccaaa tgtagtttta      666
tactacttcc ataaaacagg attggtgaat cacggacttc tagtcaacct acagcttaat      726
tattcagcat ttgagttatt gaaatcctta ttatctctat gtaaataaag tttgttttgg      786
acctcaaaaa aaaaaaa      803

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<210> 315

<211> 823

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 175..336

<221> sig_peptide

<222> 175..276

<223> Von Heijne matrix

score 3.70000004768372

seq SVLVNGHLLFSSA/CS

<221> polyA_site

<222> 812..823

<400> 315

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aaggcgcgcg cgaccggcgg ctctttggcg cggattaggg ggtctcggcg agggagtcac      60
caagcttttg tgtatgtgtt ggccggttct gaagtcttga agaagctctg ctgaggaaga      120
ccaaagcagc actcgttgcc aattagggaa tggaccgttt gggttccttt agca atg      177
                               Met

atc cct ctg ata agc cac ctt gcc gag gct gct cct cct acc tca tgg      225
Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser Trp
                               -30                               -25                               -20

```



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agc ctt ata tca agt gtg ctg aat gtg ggc cac ctc ctt ttt tcc tct      273
Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser Ser
      -15                      -10                      -5
gct tgc agt gtt tca ctc gag gct ttg agt aca aga aac atc aaa gcg      321
Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys Ala
      1                      5                      10                      15
atc ata ctt atg aaa taatggcttc agattttcct gtccttgatc ccagctggac      376
Ile Ile Leu Met Lys
      20
tgctcaagaa raaatggccc ttttagaasc tgtgatggac tgtggctttg gaaattggca      436
ggatgtagcc aatcaaatgt gcaccaarac caaggaggag tgtgagaagc actatatgaa      496
gcattttcatc aataaccctc tgtttgcatc trscctgctg aacctgaaac aascagrnga      556
agcaaaaaact gctgacacag ccattccatt tcactctaca ratgaccctc cccgacckac      616
ctttgactcc ttgctttctc gggacatggc cgggtacwtg ccmgctcgag cagatttcat      676
tgaggaattht gacaattatg cagaatggga cttgagagac attgattttg ttgaagatga      736
ctcggacatt ttacatgctc tgaagatggc tgtggtagat atctatcatt ccagggtaaa      796
ggagagacaa agacgaaaaa aaaaaaa      823

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<210> 316
<211> 823
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 191..553
<221> sig_peptide
<222> 191..304
<223> Von Heijne matrix
      score 5.69999980926514
      seq LAFLSCLAFLVLD/TQ
<221> polyA_signal
<222> 766..771
<221> polyA_site
<222> 804..817

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<400> 316
aactctgcag ggctccaag gccaggcttc agggctggga ctgagtcctg aggcactggg      60
gagccatgag gggctgtggc agggaggggc aggggtgtgga aagactcccc tggggccatg      120
gtggagatgt gctgaggtct tctccctgat cgtcttctcc tccctgctga ccgacggcta      180
ccagaackag atg gag tct ccg cag ctc cac tgc att ctc aac agc aac      229
      Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
      -35                      -30
agc gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc ctc      277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
      -25                      -20                      -15                      -10
agc tgc ctg gcc ttc ctc gtc ctg gac aca cag gag acc cgc att gcc      325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
      -5                      1                      5
ggc acc cgc ttc aag aca gcc ttc cag ctc ctg gac ttc atc ctg gct      373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala
      10                      15                      20

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gtt ctc tgg gca gtt gtc tgg ttc atg ggt ttc tgc ttc ctg gcc aac      421
Val Leu Trp Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn
    25                      30                      35
caa tgg cag cat tcg ccg ccc aaa gar kkc ctc ctg ggg agc agc agt      469
Gln Trp Gln His Ser Pro Pro Lys Glu Xaa Leu Leu Gly Ser Ser Ser
    40                      45                      50                      55
gcc cag gca gcc atc ggc stt cac ctt ctt ctc cat cct tgt ctg gat      517
Ala Gln Ala Ala Ile Gly Xaa His Leu Leu Leu His Pro Cys Leu Asp
                      60                      65                      70
att cca rgc cta cct ggc akk cca gga cct ccg aaa tgatgctcca      563
Ile Pro Xaa Leu Pro Gly Xaa Pro Gly Pro Pro Lys
                      75                      80
gtcccttacm arcgcttcct ggatgaaggt ggcattggtgs kkaacaccct ccccttgccc      623
tctgccaaca gctgtgaac atgcccacca ctggcccccag cagcctgagt tatgctagct      683
ctgccctgtc cccctgtctg accgctcmaa agtcccccccg gcttgctatg atgcctgaca      743
actaaaatc cttatccaaa tcaataaaga gagaatcctc cctccagaag ggtttctaaa      803
aacaaaaaaaa aaahncctt      823

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<210> 317
<211> 1112
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 106..603
<221> sig_peptide
<222> 106..216
<223> Von Heijne matrix
      score 4.30000019073486
      seq LWEKLTLLSPGIA/VT
<221> polyA_site
<222> 1102..1112

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<400> 317
agcgattgcg aatcctccgc tgaggtgatt tggatatccc tagaacgttg agggcacgag      60
tcgggtcctg agaccaggtc ctcagccagc agagccacgt tcctt atg agc acc gtg      117
                      Met Ser Thr Val
                      -35
ggt tta ttt cat ttt cct aca cca ctg acc cga ata tgc ccg gcg cca      165
Gly Leu Phe His Phe Pro Thr Pro Leu Thr Arg Ile Cys Pro Ala Pro
                      -30                      -25                      -20
tgg gga ctc cgg ctt tgg gag aag ctg acg ttg tta tcc cca gga ata      213
Trp Gly Leu Arg Leu Trp Glu Lys Leu Thr Leu Leu Ser Pro Gly Ile
                      -15                      -10                      -5
gct gtc act ccg gtc cag atg gca ggc aag aag gac tac cct gca ctg      261
Ala Val Thr Pro Val Gln Met Ala Gly Lys Lys Asp Tyr Pro Ala Leu
    1                      5                      10                      15
ctt tcc ttg gat gag aat gaa ctc gaa gag cag ttt gtg aaa gga cac      309
Leu Ser Leu Asp Glu Asn Glu Leu Glu Glu Gln Phe Val Lys Gly His
                      20                      25                      30
ggt cca ggg ggc cag gca acc aac aaa acc agc aac tgc gtg gtg ctg      357
Gly Pro Gly Gly Gln Ala Thr Asn Lys Thr Ser Asn Cys Val Val Leu

```

```

      35              40              45
aar mac atc ccc tca ggc atc gtt gta aag tgc cat cag aca aga tca      405
Lys Xaa Ile Pro Ser Gly Ile Val Val Lys Cys His Gln Thr Arg Ser
      50              55              60
gtt gat cag aac aga aag cta gct cgg aaa atc cta caa gag aaa gta      453
Val Asp Gln Asn Arg Lys Leu Ala Arg Lys Ile Leu Gln Glu Lys Val
      65              70              75
rat gtt ttc tac aat ggt gaa aac agt cct gtt cac aaa gaa aaa cga      501
Xaa Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His Lys Glu Lys Arg
      80              85              90              95
gaa gcg gcg aag aaa aaa car gaa agg aaa aaa aga gca aag gaa acc      549
Glu Ala Ala Lys Lys Lys Gln Glu Arg Lys Lys Arg Ala Lys Glu Thr
      100              105              110
ctg gaa aaa aag aas ctm ctt aaa raa ctg tgg gag tca agt aaa aag      597
Leu Glu Lys Lys Xaa Leu Leu Lys Xaa Leu Trp Glu Ser Ser Lys Lys
      115              120              125
gtc cac tgagaaaaga attagagatt ccaactgaca gaatctgccca gaagctccca      653
Val His
gggaataatg gtggcgagtt ccatcaccag cattattata gtgcttcaaa agaaatattt      713
ttgatgaact taaaagacaa caaattttatt taaatgggtgc actaaactgt agtgaacaga      773
gacatgcacg attcaagaat aaaactcggc cgggcacggt ggacggtgcc tcacatctgt      833
aatcccgaca ctttgggagg ccgaggcggt cggatcactt gaggtcagga gtttgagacc      893
agcctggcca acatggtgaa acccgcgtctc tactaaaaat acaaaaaatt agccaggcat      953
ggtagggggc acctgtaatc ccagctactc gggaggccga ggcaggagaa ttgcgtgaac      1013
ctgggaggcg gaggttgtag tgagctgaga tcgcgccact gcactcaagc ctgggcaaca      1073
cctgggtgac agagcaagac cccatcycaa aaaaaaaaaa      1112

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<210> 318
<211> 1623
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 47..586

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<221> sig_peptide
<222> 47..124
<223> Von Heijne matrix
      score 6.30000019073486
      seq GVGLVTLLGLAVG/SY

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```

<221> polyA_signal
<222> 1583..1588

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<221> polyA_site
<222> 1614..1623

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```

<400> 318
agggatctgt cggcttgtca ggtggtggag gaaaaggcgc tccgtc atg ggg atc      55
                                   Met Gly Ile
                                   -25
cag acg agc ccc gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act      103
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr
      -20              -15              -10

```

ctg ctc ggc ctg gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg	151
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg	
-5 1 5	
cct cag gtc act ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg	199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu	
10 15 20 25	
cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc	247
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala	
30 35 40	
ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc	295
Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile	
45 50 55	
tac ctc tcc acm mga att gat ggc agc ctg gtc atc agg cca tac act	343
Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr	
60 65 70	
cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc mtc aag	391
Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Xaa Lys	
75 80 85	
gtc tac ctg aag ggt gtg cac ccc aaa ttt cct gag gga ggg aar atg	439
Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met	
90 95 100 105	
cct cak tac ctg gat asc ctg aaa gtt ggg gat btg gtg gaa ttt csg	487
Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val Glu Phe Xaa	
110 115 120	
ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att	535
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile	
125 130 135	
cag ccc aac aag aat ctc cac cag aac ccc gag tgg cga aga aac tgg	583
Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg Arg Asn Trp	
140 145 150	
gaa tgattgccgg cgggacagga atcaccccaa tgctacagct gatccgggcc	636
Glu	
atcctgaaag tccctgaaga tccaacccag tgctttctgc tttttgccaa ccagacagaa	696
aaggatatca tcttgcgga ggacttagag gaactgcagg cccgctatcc caatcgcttt	756
aagctctggt tcaactctgga tcatccccc aaagrtrtggg cctacagcaa gggctttgtg	816
actgccgacw tgatccggga acacctgccc gctccagggg atgatgtgct ggtactgctt	876
tgtggggcmc cccaatggt gcagctggcc tgccatccca acttggacaa actgggctac	936
tcacaaaaga tgcgattcac ctactgagca tcctccagct tccctgggtgc tgctcgctgc	996
agtgtgtccc catcagtagt caagcactak aagccttagr ktcctkctct cagagtttca	1056
ggtttttttca gttrsatcka gagctgaaat ctggatagta cctgcaggaa caatattcct	1116
gtagccatgg aagagggcca aggcctcagtc actccttgga tggcctccta aatctccccg	1176
tggcaacagg tccaggagag gcccatggag cagtctcttc catggagtaa gaaggaagg	1236
agcatgtacg cttggtccaa gattggctag ttccttgata gcatcttact ctcaccttct	1296
ttgtgtctgt gatgaaagga acagtctgtg caatggggtt tacttaaaact tcaactgttca	1356
acctatgagc aaatctgtat gtgtgagtat aagttgagca tagcatactt ccagaggtgg	1416
tcttatggag atggcaagaa aggaggaaat gatttcttca gatctcaaag gagtctgaaa	1476
tatcatattt ctgtgtgtgt cdctctcagc cctgcccad gctagaggga wacagctact	1536
gataatcgaa aactgctgtt tgtgggcarg aaccctggc tgtgcaaata atggggctga	1596
ngccctgtgt gatattgaaa aaaaaaa	1623

<210> 319

<211> 526

<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> 99..371

<221> sig_peptide
<222> 99..290
<223> Von Heijne matrix
score 3.79999995231628
seq LFIVVCVICVTLN/FP

<221> polyA_signal
<222> 491..496

<221> polyA_site
<222> 513..524

<400> 319
attggattag tagaattgct tttgtcattc cattgttttc atatatttgt ttgggacatt 60
ttactttttt ctgttaacgc ttaccctagr aattagaa atg aca cca cgt att ctt 116
Met Thr Pro Arg Ile Leu
-60
agc gaa gtc cag ttt tca gca ttt tgt cct tat tgg aca ata gca agg 164
Ser Glu Val Gln Phe Ser Ala Phe Cys Pro Tyr Trp Thr Ile Ala Arg
-55 -50 -45
ata tta gaa cgt gtt ggt tcc gcg tgc ttc cgt ctt gag tta tgt gct 212
Ile Leu Glu Arg Val Gly Ser Ala Cys Phe Arg Leu Glu Leu Cys Ala
-40 -35 -30
gct att gtc gga tat ttt gtc tta gat gta cgt act ttc ctg ttc att 260
Ala Ile Val Gly Tyr Phe Val Leu Asp Val Arg Thr Phe Leu Phe Ile
-25 -20 -15
gtg gta tgt gta att tgc gtt act ttg aat ttt cca cgt ttt tac ttt 308
Val Val Cys Val Ile Cys Val Thr Leu Asn Phe Pro Arg Phe Tyr Phe
-10 -5 1 5
ctt tgt ctc tca tca ctt acc gct ttt ggg acc ccc ccc atc ggg gtt 356
Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly Thr Pro Pro Ile Gly Val
10 15 20
cac att ccc tct ccc tararcacac tcccttgat ttcctcradt ggggtctgct 411
His Ile Pro Ser Pro
25
gcggtgaagc tttccattt tatgtgcaga ttattttcag agggatatata gaattcaggc 471
agctgtttcg ttgtagcaca ttaaaaaatat tttcccactt caaaaaaaaa aaacc 526

<210> 320
<211> 989
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..814

<221> sig_peptide
<222> 44..112
<223> Von Heijne matrix
score 8.30000019073486

seq VRLLXLLLLLLIA/LE

<221> polyA_site

<222> 978..989

<400> 320

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aaatgtgtac acgcccagct tcctgcctgt tactctccac agt atg cga aga ata      55
                                   Met Arg Arg Ile
                                   -20
tcc ctg act tct agc cct gtg cgc ctt ctt ttg tdt ctg ctg ttg cta      103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Leu Leu Leu
                                   -15      -10      -5
cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac      151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
                                   1      5      10
ttc act ata aaa tca ttg tcc aga cct gga cag ccc tgg tgt gaa gcg      199
Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala
                                   15      20      25
cat gtc ttc ttg aat aaa aat ctt ttc ctt cag tac aac agt gac aac      247
His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn
                                   30      35      40      45
aac atg gtc aaa cct ctg ggc ctc ctg ggg aag aag gta tat gcc acc      295
Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr
                                   50      55      60
agc act tgg gga gaa ttg acc caa acg ctg gga gaa gtg ggg cga gac      343
Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp
                                   65      70      75
ctc agg atg ctc ctt tgt gac atc aaa ccc car ata aag acc agt gat      391
Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile Lys Thr Ser Asp
                                   80      85      90
cct tcc act ctg caa gtc kar atk ttt tgt caa cgt gaa gca gaa cgg      439
Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg Glu Ala Glu Arg
                                   95      100      105
tgc act ggt gca tcc tgg cag ttc gcc acc aat gga gag aaa tcc ctc      487
Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly Glu Lys Ser Leu
                                   110      115      120      125
ctc ttt gac gca atg aac atg acc tgg aca gta att aat cat gaa gcc      535
Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile Asn His Glu Ala
                                   130      135      140
agt wag atc aag gag aca tgg aag aaa gac aga ngg ctg gaa aak tat      583
Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa Leu Glu Xaa Tyr
                                   145      150      155
ttc agg aag ctc tca aar gga gac tgc gat cac tgg ctc agg gaa ttc      631
Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp Leu Arg Glu Phe
                                   160      165      170
tta ggg cac tgg gaa gca atg cca raa ccg ama gtg tcm cca rta aat      679
Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val Ser Pro Xaa Asn
                                   175      180      185
gct tca raw atc cac tgg tct tct tct art cta cca raw ara tgg atc      727
Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro Xaa Xaa Trp Ile
                                   190      195      200      205
atc ctg ggg gca ttc atc ctg tta vtt tta atg gga att gtt ctc atc      775
Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly Ile Val Leu Ile
                                   210      215      220
tgt gtc tgg tgg caa aat ggc ara ara tcc acc tad arg tgataccacg      824
Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa Xaa
                                   225      230

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gcggcgcaaaa attgttcacc tgtggtcctc gatcgtgac agccttggt cccactgctg	884
tgtgttcctt gagtcaagtg gaggcggagc ctgcaatgag cggaratcgc gcctctgcat	944
tccagtcttg gcaacagarc aagactccgt ctcaaaaaaa aaaaa	989

<210> 321
<211> 1017
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 3..581

<221> sig_peptide
<222> 3..182
<223> Von Heijne matrix
score 6.69999980926514
seq LWPFLTWINPALS/IC

<221> polyA_site
<222> 1006..1016

<400> 321	
ac atg tgc cct agt ctg gaa gag gct ccc agt gtc aag ggg act ctg	47
Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu	
-60 -55 -50	
ccc tgc tca gga caa cag cag cct ttc ccg ttt gga gcc tca aac atc	95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile	
-45 -40 -35 -30	
cca cta ctc ctg ggc agg agc aga aag gtg gct cga ggt gca ccg gtc	143
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val	
-25 -20 -15	
ctg tgg cca ttt ctc act tgg ata aac cct gca ctg tcc atc tgt gac	191
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp	
-10 -5 1	
ccc tta gga tcc tgc gga tgg cyw tgc cac acg gcc car gtc cct gcg	239
Pro Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala	
5 10 15	
ccc ctg car ttg cct act gcc tgt cct ccc ctc cca cat ggc acc cgg	287
Pro Leu Gln Leu Pro Thr Ala Cys Pro Pro Leu Pro His Gly Thr Arg	
20 25 30 35	
gct gta ggc ccc acg cca ggc ctc ctc cct gag gct gca gcc cca sgc	335
Ala Val Gly Pro Thr Pro Gly Leu Leu Pro Glu Ala Ala Ala Pro Xaa	
40 45 50	
acg tgk ggg gca ctg tcc tca cgc agc agg cac tgg tca tgt tcc att	383
Thr Xaa Gly Ala Leu Ser Ser Arg Ser Arg His Trp Ser Cys Ser Ile	
55 60 65	
gtc arc tgc ctc cac ctg cac ara ctc ctg tct gtg gag acc aga arc	431
Val Xaa Cys Leu His Leu His Xaa Leu Leu Ser Val Glu Thr Arg Xaa	
70 75 80	
ttc cas aaa cat ctg ttg gtg ctg ctg gtg gct gtg gcc cat agt gtt	479
Phe Xaa Lys His Leu Leu Val Leu Leu Val Ala Val Ala His Ser Val	
85 90 95	
ctg gaa cca cct gcc ctg gtc cca aat gtg cag tgt gag atg tgc aca	527
Leu Glu Pro Pro Ala Leu Val Pro Asn Val Gln Cys Glu Met Cys Thr	

100	105	110	115	
cac tca ggg ccc cgt gac ctg gaa gcc gca gtc gtg tcc cca gca cct				575
His Ser Gly Pro Arg Asp Leu Glu Ala Ala Val Val Ser Pro Ala Pro				
	120	125	130	
tgg gaa tgagcctgtc ctctgtgtga aggaggggggt gggttctcaaa ccactgactc				631
Trp Glu				
ttggtgctca ggagggggcct gctgctgtcc tgggcatggg gtggtcattg ttcaagactg				691
aggcagactc agtctttgaa aggggtgcaga ggccaggcgc ggtgggtcac gcctgtaatt				751
ccagcacttt gggaggccaa ggtggacaga tcatgaggtc aggagtcca gaccagcctg				811
gccaatacgg tgaaaccgca tctctactaa rraatawcaw aaattagtcg ggcatgggtg				871
atgtgtgctt gtagtcccag ctactcatga ggyctgaggc agaagaatca cctgaatctg				931
ggaggcagag gttgcagtga accaagatcg cacgactgta caccagcctg ggcgacagag				991
tgagactccg tctcaaaaaa aaaaam				1017

<210> 322
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..427
 <221> sig_peptide
 <222> 107..190
 <223> Von Heijne matrix
 score 3.79999995231628
 seq RFLSLSAADGSDG/SH
 <221> polyA_signal
 <222> 499..504
 <221> polyA_site
 <222> 516..529
 <400> 322

aaagtcagcg ctggagtcgg ctaggcggct ggaaacggcg gctgccgccg gtgactcagg	60
gaggcggggag gccgmsggmg gagctcttcc tgcaggcgtg garacc atg gtg ctc	115
	Met Val Leu
acg ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt	163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser	
-25 -20 -15 -10	
ctg tcc gca gcc gac ggc agc gat ggc agc cac gac agc tgg gac gtg	211
Leu Ser Ala Ala Asp Gly Ser Asp Gly Ser His Asp Ser Trp Asp Val	
-5 1 5	
gag cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt	259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val	
10 15 20	
tcc cac acc gac gtt acc aag aag gat ctg aag gtg tgt gtg gaa ttt	307
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys Val Cys Val Glu Phe	
25 30 35	
gak ggg gaa tct tgg agg aaa aga aga tgg ata gaa gtc tac agc ctt	355
Xaa Gly Glu Ser Trp Arg Lys Arg Arg Trp Ile Glu Val Tyr Ser Leu	
40 45 50 55	
cta agg aaa gca ttt tta gta aaa cat aat ttg gtt tta gct gaa cga	403

Leu Arg Lys Ala Phe Leu Val Lys His Asn Leu Val Leu Ala Glu Arg	
60 65 70	
aag tca cct gaa att tct tgg ggt taaccatctt tagttaaatg gaattttaat	457
Lys Ser Pro Glu Ile Ser Trp Gly	
75	
ttaaattgacg ctttgctaatt tttaagtgtt aagcattttg cattaaaata ttcataataat	517
aaaaaaaaaa aa	529

<210> 323
 <211> 1046
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..407

<221> sig_peptide
 <222> 45..83
 <223> Von Heijne matrix
 score 5.69999980926514
 seq MLVLRSA/ALTRALA/SR

<221> polyA_signal
 <222> 1008..1013
 <221> polyA_site
 <222> 1032..1042

<400> 323	
aaaaggacac ggctggctgc ttttctcagc gccgaagccg cgcc atg ctc gtc ctc	56
Met Leu Val Leu	
-10	
aga agc gcc ctg act cgg gcg ctg gcc tca cgg acg ctg gcg cct cag	104
Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr Leu Ala Pro Gln	
-5 1 5	
atg tgc tca tct ttt gct acg gga ccc aga caa tac gat gga ata ttc	152
Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr Asp Gly Ile Phe	
10 15 20	
tat gaa ttt cgt tct tat tac ctt aag ccc tca aag atg aat gag ttc	200
Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys Met Asn Glu Phe	
25 30 35	
ctg gaa aat ttt gag aaa aac gct caa ctt cgg aca gct cac tct gaa	248
Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr Ala His Ser Glu	
40 45 50 55	
ttg gtt gga tac tgg agt gta kaa ttt gga ggc aga atg awt aca gtg	296
Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg Met Xaa Thr Val	
60 65 70	
ttt cat att tgg aag tat gat aat ttt gct cat cga act gaa ttt cag	344
Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Glu Phe Gln	
75 80 85	
aaa gcc ttg gcc aaa gat aag gaa tgg caa gaa caa ttc ctc att cca	392
Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Pro	
90 95 100	
aat ttg gct ctc aat tgataaaciaa gatagtgaga ttacttatct ggtaccatgg	447

Asn Leu Ala Leu Asn

105

tgcaaatag	aaaaacctcc	aaaagaagga	gtctatgaac	tggccacttt	tcagatgaaa	507
cctgggtgggc	cagctctgtg	gggtgatgca	tttaaaaggg	cagttcatgc	tcagtgtcaat	567
ctaggctaca	caaaactagt	tggagtgttc	cacacagagt	acggagcact	caacagagtt	627
catgttcttt	ggtggaatga	gagtgcagat	agtcgtgcag	ctgggagaca	taagtcccat	687
gaggatccca	gagttgtggc	agctgttcgg	gaaagtgtca	actacctagt	atctcagcag	747
aatatgcttc	tgattcctac	atcgttttca	ccactgaaat	agttttctac	tgaaatacaa	807
aacatttcat	taactgctat	aggatctgtc	tgctaattgg	gcttaaattc	tccaagagg	867
ttctcacttt	tatttgaagg	aggtggttaag	ttaatttgct	atgtttcttg	cattatgaag	927
gctacatctg	tgctttgtaa	gtaccacttc	aaaaaatakt	tctgtttact	ttctgcatgg	987
tatttcagtg	tctgtcatat	attaaaaata	ctgtgcactg	tttyaaaaaa	aaaaammcc	1046

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<211> 880

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 201..332

<221> sig_peptide

<222> 201..251

<223> Von Heijne matrix

score 7.80000019073486

seq VLWLISFFFTFDG/HG

<221> polyA_site

<222> 869..880

<400> 324

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gatactttct	ttccaaacag	cataagaagt	gattgancca	caagtatact	gaaggmargg	120
yhcccwswar	tyctggwgtg	amgagataaa	tcaccagtca	cagactatgc	acccgactgc	180
tgctgttcag	tccagggaaa	atg aaa gtt	gga gtg ctg	tgg ctc att	tct ttc	233
Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe						
-15 -10						
ttc acc ttc	act gac ggc	cac ggt ggc	ttc ctg ggg	gtg agt tgg	tgc	281
Phe Thr Phe	Thr Asp Gly	His Gly Gly	Phe Leu Gly	Val Ser Trp	Cys	
-5 1 5 10						
tat gtc tca	tat ctc ttc	tca act aac	tct cct ctc	tcg ttc	cgg cgc	329
Tyr Val Ser	Tyr Leu Phe	Ser Thr Asn	Ser Pro Leu	Ser Phe Arg	Arg	
15 20 25						
att tagaaccct	cactctctag	gggactgcaa	ctgcataatt	taatgtactt		382
Ile						
gagatcagaa	gtcctgagtt	ctcgtttcaa	cattaccaac	attcactgtg	tggccttgga	442
taagtragtc	atttcatctc	ttcggagctt	agatgatcma	actgcaarag	gaggatcttt	502
gattamacta	tcttagagat	cttttccagt	tcaacacatg	ctgtactatg	gcttctcggg	562
tgcagaaaaa	tcacatggat	ggacattagc	aatccttara	cactgtcttt	cctgtctaca	622
ctcgcttgag	tgatgckttc	atctaggatc	atggttttaa	tattctctac	atgctgatga	682
ctcccagctg	tatagctcca	tctcagaacc	tctcccctgt	ccacactcac	atatccatta	742
cctacgtgtt	atttccagct	gggaaatcca	gcggaacctc	ggnaacttca	tttgnttcaa	802
aatcgnaacc	caatccttct	tgccctatctc	agcaagtggg	atcactatct	ttccagctac	862
ttaggcaaaa	aaaaaaaa					880

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 <212> DNA
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 <222> 217..543

<221> sig_peptide
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 <223> Von Heijne matrix
 score 6.40000009536743
 seq MCLLTALVTQVIS/LR

<221> polyA_site
 <222> 1206..1217

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graagrwwga aasctgtcta aaaatattca agtgtgcaac caaggattta gatgaagcca      180
gcaaacaaag gaatcatgta atcaggacct gagcga atg tgc tta ctc acg gcg      234
                               Met Cys Leu Leu Thr Ala
                               -10
tta gtt aca cag gtg att tcc tta aga aaa aat gca gag aga act tgt      282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
-5                               1                               5
tta tgc aag agg aga tgg ccc tgg ngc ccc tgc ccc cgg atc tac tgc      330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
10                               15                               20                               25
tca tcc acc cca tgc gat tcc aaa ttc ccc acc gtc tac tcc agt gcc      378
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser Ala
30                               35                               40
cca ttc cat gcc ccc ctc ccc gtc cag aat tcc tta tgg ggg cac ccg      426
Pro Phe His Ala Pro Leu Pro Val Gln Asn Ser Leu Trp Gly His Pro
45                               50                               55
ctc cat ggt tgt tcc tgg caa tgc cac cat ccc cag gga car aat ctc      474
Leu His Gly Cys Ser Trp Gln Cys His His Pro Gln Gly Gln Asn Leu
60                               65                               70
cag cct gcc agt ctc cad acc cat ctc tcc aag ccc aag cgc cat ttt      522
Gln Pro Ala Ser Leu Xaa Thr His Leu Ser Lys Pro Lys Arg His Phe
75                               80                               85
ara aar aar rra tgt caa gcc tgatgaarac atgagtggca aaaacattgc      573
Xaa Lys Lys Xaa Cys Gln Ala
90                               95
aatgtacara aatgagggtt tctatgctga tccttacctt tatcacgagg gacggatgag      633
catascctca tcccatgggtg gacacccact ggatgtcccc gaccacatca ttgcatatca      693
ccgcaccgcc atccgggtcag cgagtgtcta ttgtaacccc tcaatgcaag cggaaatgca      753
tatggaacaa tcaactgtaca gacagaaatc aaggaaaatat ccggatagcc atttgcctac      813
actgggctcc aaaacacccc ctgcctctctc tcacagaktc agtgacctga ggatgataga      873
catgcacgct cactataatg cccacggccc ccctcacacc atgcagccag accgggcctc      933
tccgagccgc caggccttta aaaaggagcc aggcaccttg gtgtatatag aaaagccacg      993
gagcgtctga ggattatcca gcctttaga cctcggccct cctctaattgg agaagcaagt     1053
    
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ttttgcctac agcacggcga caatacccaa agacagagag accagagaga ggatgcaagc 1113
catggagaaa cagattgccca gtttaactgg ccttggttcag tctgcgcttt ttaaagggcc 1173
cattacaagt tatagcaaar atgcgtctag ctaaaaaaaa aaaa 1217
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<210> 326
<211> 959
<212> DNA
<213> Homo sapiens

<220>
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<222> 18..446

<221> sig_peptide
<222> 18..140
<223> Von Heijne matrix
score 4.099999990463257
seq GILILWIIRLLFS/KT

<221> polyA_signal
<222> 930..935

<221> polyA_site
<222> 948..959

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-40 -35
gag atg gta cag gcg ctt tac gag gct cct gct tac cat ctt att ttg 98
Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu
-30 -25 -20 -15
gaa ggg att ctg atc ctc tgg ata atc aga ctt ctt ttc tct aag act 146
Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr
-10 -5 1
tac aaa tta caa gaa cga tct gat ctt aca gtc aag gaa aaa gaa gaa 194
Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu
5 10 15
ctg att gaa gag tgg caa cca gaa cct ctt gtt cct cct gtc cca aaa 242
Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys
20 25 30
gac cat cct gct ctc aac tac aac atc gtt tca ggc cct cca agc cac 290
Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His
35 40 45 50
aaa act gtg gtg aat gga aaa gaa tgt ata aac ttc gcc tca ttt aat 338
Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn
55 60 65
ttt ctt gga ttg ttg gat aac cct agg gtt aag gca gca gct tta gca 386
Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala
70 75 80
tct cta aag aag tat ggc gtg ggg act tgt gga ccc tgt gga ttt tat 434
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys Gly Phe Tyr
85 90 95
ggc aca ttt gaa tgaaratgaa ggatcattga tttccttggtg tatggataat 486
Gly Thr Phe Glu

100

ccgggaacag	gccaaactaaa	tatttgatga	atgtatgatt	tcaaatacag	tgaattccct	546
gggagtcac	aaaraagacg	gcatttttatg	gttggtttta	ttaagtgtat	attctttgct	606
cctgaaaatg	ttattaaata	attgttttagg	ccgggcatgg	tggctcatgc	ctgtaatccc	666
agcactttca	aaggctgagg	caggcagatc	acctgaggtc	aggagttcaa	aaccagcctg	726
gccaacatgc	tgaaacctcg	tctctactaa	aaatacaaaa	attagctggg	cgtgggtggg	786
grtgctgtg	gtcccagctr	cgtgggaggc	tgaggtggga	gaattgcttc	aacctgggag	846
gcggaggttg	cagtgagccg	agatcatgcc	actgcactcc	agcctgggca	acagagcaag	906
actgtctcaa	aaataaataa	ataaataaaa	ttgttttaaat	gaaaaaaaaa	aaa	959

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 <211> 921
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..724

<221> sig_peptide
 <222> 29..118
 <223> Von Heijne matrix
 score 3.90000009536743
 seq VAHALSLPAESYG/NX

<221> polyA_signal
 <222> 886..891

<221> polyA_site
 <222> 910..920

<400> 327

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			-30 -25	
gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg ctt tct ctc	100			
Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala Leu Ser Leu				
-20 -15 -10				
cca gca gag tcg tat ggy aac grt yct gac att gag atg gct tgg gcc	148			
Pro Ala Glu Ser Tyr Gly Asn Xaa Xaa Asp Ile Glu Met Ala Trp Ala				
-5 1 5 10				
atg aga gca atg cag cat gct gaa gtc tat tac aag ctg att tca tca	196			
Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu Ile Ser Ser				
15 20 25				
gtt gac cca cag ttc ctg aaa ctc acc aaa gta gat gac caa att tac	244			
Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp Gln Ile Tyr				
30 35 40				
tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat gtg ttg grc	292			
Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp Val Leu Xaa				
45 50 55				
cca gaa gan ctc aag tca gaa tca gcn aaa gag ccc cca gga tac aat	340			
Pro Glu Xaa Leu Lys Ser Glu Ser Ala Lys Glu Pro Pro Gly Tyr Asn				
60 65 70				
tct ttg cca ttg aaa ttg ctc gga acc ggg aag gct ata aca aag ctg	388			
Ser Leu Pro Leu Lys Leu Leu Gly Thr Gly Lys Ala Ile Thr Lys Leu				

75	80	85	90	
ttt ata tca gtg ttc agg aca aag aag gag aga aag gag tca aca atg				436
Phe Ile Ser Val Phe Arg Thr Lys Lys Glu Arg Lys Glu Ser Thr Met				
	95	100	105	
gag gag aaa aaa gag ctg aca gtg gag aag aag aga aca cca aga atg				484
Glu Glu Lys Lys Glu Leu Thr Val Glu Lys Lys Arg Thr Pro Arg Met				
	110	115	120	
gag gag aga aag gag ctg ata gtg gag aag aaa aag agg aag gaa tca				532
Glu Glu Arg Lys Glu Leu Ile Val Glu Lys Lys Lys Arg Lys Glu Ser				
	125	130	135	
aca gag aag aca aaa ctg aca aag gag gag aaa aag gga aag aag ctg				580
Thr Glu Lys Thr Lys Leu Thr Lys Glu Glu Lys Lys Gly Lys Lys Leu				
	140	145	150	
aca aag aaa tca aca aaa gtg gtg aaa aag cta tgt aag gta tac agg				628
Thr Lys Lys Ser Thr Lys Val Val Lys Lys Leu Cys Lys Val Tyr Arg				
	155	160	165	170
gaa cag cac tct aga agc tat gac tca att gag act aca agt acc acg				676
Glu Gln His Ser Arg Ser Tyr Asp Ser Ile Glu Thr Thr Ser Thr Thr				
	175	180	185	
gtg cta ctt gca cag acc cct ttg gtt aaa tgt aaa ttc ttg tac aat				724
Val Leu Leu Ala Gln Thr Pro Leu Val Lys Cys Lys Phe Leu Tyr Asn				
	190	195	200	
ctgaaggatac gcagaaggac atcttttctag tctaacagtc aggagctgct ctgggtcattc				784
ccttgtatga actggtctaa agactgttag tgggggtgta gttgattttt cctgggtatac				844
ctgttttcttgg ctgacactac tgggtcaagta agaaatttgt aaataaattt ctttttggttc				904
ttattaamaa aaaaaaas				921

<210> 328
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 404..586

<221> sig_peptide
 <222> 404..466
 <223> Von Heijne matrix
 score 4.09999990463257
 seq SLMFFSMMATCTS/NV

<221> polyA_signal
 <222> 1304..1309

<221> polyA_site
 <222> 1334..1344

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aattccacaa tagttgagaa aaatgagcat ttttttccat ttttaaaaaa tgcataagaaa	120
agacaatttt aaaatcctgg gamccawatt tatttagaag tagctgttag taaaacatta	180
gaaaaggagt caggccatba ggttatttat nbnaatctct aagcaattag gntgaagtta	240
ttaagtcaag cctagaaaag ctgccttcctt gtaaggcttt catgacaatg tatagtaatc	300
brcagtggtcc aattcttcgc actcctcagg aatatcacta cctcagggtta cggtagacag	360

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gctataattg atgatgatgt tcagataact gaagacacaa taa atg aca ttc aga      415
                               Met Thr Phe Arg
                               -20
cat cag gac aat tcc ctc atg ttc ttt tct atg atg gcc acc tgt acc      463
His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met Ala Thr Cys Thr
      -15                      -10                      -5
agc aac gtg ggt ttc acc cac aca acg atg aac tgt tct ctt act tct      511
Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys Ser Leu Thr Ser
      1                      5                      10                      15
cca gtt gat ttt aaa gac ttg tta aga gtc tta cta ata aaa ttt ggg      559
Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu Ile Lys Phe Gly
      20                      25                      30
tat gat aga aaa tcc aca atc aaa tct tgaaccaa aacatattaa      606
Tyr Asp Arg Lys Ser Thr Ile Lys Ser
      35                      40
attactaata ttttaagtgat ggaagacaca caaaaaactt aaaagcacga acaacctaac      666
ttgaaaaara atttttaaat atgattaacc tgaaraaaaa araatcctaa ragccaaagc      726
tcctttttat ttagcttgga attttcctat tggttcctaa caaactgtcc caatgtcata      786
taaggaaaca tgatctatta cattccttta taacaacgtg gararactat aaacctatgt      846
aagtagtaaaa actatatcag adactcagga ractgactww aaggcctgga tctgcagtgt      906
attatctgta taaaaattgg cagggggaag ctaaaaggaa aggagattgg agatctcaat      966
tctatcatgg tgtatttcat acgcaaatca ragcatgcat tgttttttgt ttttggaar      1026
avaarggaag tgtgttctgc cccatgtttc cttccgtgtt tatagttcaa actctatata      1086
tacttcaggt attttttgtt tagcccttca ttataaatgg gcaggaaatt gtttatcaac      1146
ctagccagtt tattactagt gaccttgact tcagtatcct gagcattcct ttatatTTTT      1206
cttttattat cctgagtctg taactaaaca attttgtcct caaattttta tccaatatcc      1266
attgcaccac accaaatcaa gcttcttgat tttcaaaaat aaaaaggggg aaatacttac      1326
aacttgtaaa aaaaaaaaaa                                1344

<210> 329
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 331..432

<221> sig_peptide
<222> 331..387
<223> Von Heijne matrix
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      seq AGLSSCLLPLCWL/ER

<221> polyA_signal
<222> 548..553

<221> polyA_site
<222> 573..585

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gcgcgggass ggtgccagtc tttaaacaac ctctcgatgg gtccacagaa gatgtttcca      120
gacccttggg atgccaagtt caagtttagc tatgtctcgc ggagaggccg gtggaagaag      180
caacgagaat gaagcacccc agttctctgc tgagcacatg ggcattctgca ataaagattt      240

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aatttccag cttctcctga agctcggat ggccacaaca ctaaattctg cccgaggaga 300
ttgagcaaaa tagtatggga cttccaagaa atg ttt tta aag tca ggg gca ggc 354
                                Met Phe Leu Lys Ser Gly Ala Gly
                                -15
ctt tct tca tgc ctt ctt cct ctt tgc tgg ctg gaa cgc aaa gac cat 402
Leu Ser Ser Cys Leu Leu Pro Leu Cys Trp Leu Glu Arg Lys Asp His
-10 -5 1 5
ggc agg agg cca agc asc cat cct gga agg tgaaagcctc atactaagga 452
Gly Arg Arg Pro Ser Xaa His Pro Gly Arg
10 15
cgtcaracag cgaaataara rcctgggtcc ttgaccctgt aaasatctcc ctccccatcc 512
tggtctgtct gccttgactc ctttcatatg aaaaaaataa actttttaact tgcgtwaacc 572
aaaaaaaaa aaa 585

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<210> 330
 <211> 914
 <212> DNA
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<220>
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score 5.09999990463257
seq FLLSQMSQHQVHA/VQ
<221> polyA_signal
<222> 886..891
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<222> 903..914
<400> 330

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atg aac rra tat gca agt cca ttc aac tgw caa ttg ard tat ttg gak 106
Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
-50 -45 -40
ttg agc agr ttc gag tgt gtr cat aga gat gga aga gta att aca ctg 154
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
-35 -30 -25
tct tat cag gag cag gag cta cag gat ttt ctt ctg tct cag atg tca 202
Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
-20 -15 -10
cag cac cag gta cat gca gtt cag caa ctc gcc aag gtt atg ggc tgg 250
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
-5 1 5 10
caa gta ctg agc ttc agt aat cat gtg gga ctt gga cct ata gag agc 298
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
15 20 25
abt ggt aat gca tct gcc atc acg gtg gcc ccc caa gtg gtg act atg 346
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
30 35 40

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cta ttt cag ttc gta atg gac ctg aaa gtg gca gca aga tta tgg ttc	394
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe	
45 50 55	
agt ttc ctc gta acc aat gta aar acc ttc caa aaa gtg atg ttt tac	442
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr	
60 65 70	
aar ata aca aat gga gtc atc ttc gtg ggc cat tca aar aag ttc agt	490
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser	
75 80 85 90	
gga ata aaa tgg aag gtc kaa att ttg ttt ata aaa tgg arm tgc tta	538
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu	
95 100 105	
tgt ctg cac tta gcc ctt gtc tac tat gat ttt ttc car atg ttt cct	586
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro	
110 115 120	
aaa raa gtt tcc ara aac ttt gac ttg aaa tgt ttg car atc aac tat	634
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr	
125 130 135	
aag cac aaa gaa gar ata act tcc aaa aga gtg ctg ttt tta aaa ata	682
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile	
140 145 150	
ata att agg aaa tgt ttt att tagcactttc aaacttttca ctttataaat	733
Ile Ile Arg Lys Cys Phe Ile	
155 160	
gacaagtgtt ttgaaatgca gaagtttatg tacagttgta tatacagtat gacaagatgt	793
aaaaataatat gtttttcatg cagtttaaaa tattactaac ttaagggttt ctatgtgctt	853
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	914

<210> 331
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 672..752

<221> sig_peptide
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 <223> Von Heijne matrix
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 seq LLYAHLSTSKRA/VV

<221> polyA_site
 <222> 1150..1161

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ctttagatg gcatatattc agcatatgtt gcatgtsttc agaattacat aagatgaaat	180
ccctttcatt gcaacttgca agtgagaaaa gatccttagt ggctctggtg gaagaaatag	240
tatttcttct tctcagggtg tctccctgcc ttggcccttc ccagaagccc cggctttaaa	300
agtgaaaatg tttgaaacat gaaacatgtc tgtaggaagc atcagcatgg ccataagtgc	360
artgattttc atatatgcct ctgcccattt caaatatatt tttagcatga ataaatctaa	420

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cagtatacar aataattcat gtaaraccct aacgtgtaca tgtgaaaaag catttctata 480
taatgtgagg agcactggcc atcaattagg gaaataaagg tcatgtaata ttgcaaattt 540
tcaaaataga gcsstgcaag ataactgcaa tcataccaaa aactatttga gtaaattgat 600
ttttaaaagta atttttgttt aaaaaaattt atatttcaga agsagaaaat gtcaaattgat 660
agtctttgta a atg gtg gtg cac ctt ctc tat gca cat ctg tct ttt aca 710
          Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr
          -15          -10          -5

tca aaa aga gct gtg gtc atg cta aaa tta gag ata act ttt 752
Ser Lys Arg Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
          1          5          10

tgaatgactt ggtcaagctg tgtgtaaaat atttaaccat aagtcaagta cagtgtacta 812
tgtttaataa agttacattt aatgcattta ttgcatatat gaatatatac atgaagaggc 872
tttatgtctt ctgggtatttg attttgaatg ttttttaagt cagtgggtgcc tttagggaag 932
aactttcgaa attaatcatt ctttgtgttt tctgattttt caggtaacat gtacactatt 992
tagaaacccat catagtttat tcaccttaaa aaattgattg tattatttaa atatatcact 1052
tagatgggca tttcctataa ttaggatatt ccaaatagtt gctgaaatca attgtgccat 1112
tgaccaatgg atgcacttgg ttagccttaa ttttttyaaa aaaaaaaaaa 1161

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<210> 332
<211> 363
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 57..311
<221> sig_peptide
<222> 57..128
<223> Von Heijne matrix
      score 5.30000019073486
      seq LFHLLFLPHYIET/FK
<221> polyA_signal
<222> 332..337
<221> polyA_site
<222> 351..363

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<400> 332
acatttctta ctgccttacg ctcatcctga ggtccacctt ggtctctaaa aacacc atg 59
                               Met

tgt tct cat gcc tcc atg tct ttt cac aca ctg ttc cat ttg ctc ttc 107
Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu Phe
          -20          -15          -10

ctc cca cat tac att gaa act ttc aag cct cag tcg aaa cat tgc ttc 155
Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys Phe
          -5          1          5

ttc tgg ata gca gcc ttc ttg aca tcc ctc ctc act ccc cag tcc cta 203
Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser Leu
10          15          20          25

cag ggc ttc cat agc tct tta tgt gca ctt cga tcc cag cat ttt cca 251
Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe Pro
          30          35          40

tcg act tgt aat tgt ttc tgc tac ctg aca atc atc gcc ttg drd tac 299

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```

Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa Tyr
      45              50              55
tgg gac aac ctt tgattactca ttatatcctc aataaatatt tgttgaacca      351
Trp Asp Asn Leu
      60
aaaaaaaaaa aa      363

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<210> 333
<211> 645
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 80..232

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<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.70000004768372
      seq IALTLIPSMLSRA/AG

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<221> polyA_signal
<222> 617..622

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<221> polyA_site
<222> 634..645

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<400> 333
accttcttgt tatattatgct attctctttg ttggtccatt cttctttcaa tcttctcagc      60
ttataaccgt ctttccctt atg cta agg ata gcc ctt aca ctc atc cca tct      112
      Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser
      -15              -10
atg ctg tca agg gct gct ggt tgg tgc tgg tac aag gag ccc act cag      160
Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln
      5              1              5              10
cag ttt tct tac ctt tgc ctg ccc tgc ctt tca tgg aat aar aaa ggc      208
Gln Phe Ser Tyr Leu Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly
      15              20              25
aac gtt ttg cag ctt cca aat ttc tgaaraaaact aatctcarat tggcagttaa      262
Asn Val Leu Gln Leu Pro Asn Phe
      30              35
agtcaaaatg ttgccaaata tttattcctt ttgcctaakt ttggctaccc ggttcaattg      322
ctttttatatt ttaatgtctt gactcttcar agttcgtacc tcaaaaraac aatgaraaca      382
tttgctttgc tttctgctga atccctaatac tcaacaatat atacctggac tgtccagttc      442
tcctcctgtg ctatcttctc ttctatccaa gtaraatgta ygccaggarc tccttccctc      502
tarcaatttc tactaaaaatg tccaagtara atgtttcctt ttacaatcaa attactgtat      562
ttattaattt gctaraatcc aktaaatacat tttggtagct ctggctgtgc tatcaataaa      622
aagatgaaag caaaaaaaaaa aaa      645

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<210> 334
<211> 400
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 91..291

<221> sig_peptide

<222> 91..219

<223> Von Heijne matrix

score 3.79999995231628

seq LISVLYLIPKTLT/TN

<221> polyA_signal

<222> 367..372

<221> polyA_site

<222> 389..400

<400> 334

aacaaaagga gagttttata attcacttta aaaggagatt tgatggtaaa gtttaaagat 60

taaaatattt tgttcttcaa ttacagagcg atg acc cca cag tat ctg cct cac 114

Met Thr Pro Gln Tyr Leu Pro His

-40

ggt gga aaa tac caa gtt ctt gga gat tac tct ttg gca gtg gtc ttc 162

Gly Gly Lys Tyr Gln Val Leu Gly Asp Tyr Ser Leu Ala Val Val Phe

-35 -30 -25 -20

ccc ctg cac ttt tct gat cta att tct gtt tta tac ctt ata ccc aaa 210

Pro Leu His Phe Ser Asp Leu Ile Ser Val Leu Tyr Leu Ile Pro Lys

-15

-10

-5

aca ctt act acc aac aca gct gtt aaa cat tct ata caa aaa aat tgt 258

Thr Leu Thr Thr Asn Thr Ala Val Lys His Ser Ile Gln Lys Asn Cys

1

5

10

atg mat ctg gta tta gga aaa tta ctt tca cag taaatatcaa agaaaaaaga 311

Met Xaa Leu Val Leu Gly Lys Leu Leu Ser Gln

15

20

ttaagggtct ctttgccatg cttttcatca tatgcaccaa atgtaaattt tgtacaataa 371

aaattttattt cctaagyaaa aaaaaaaaaa 400

<210> 335

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 196..384

<221> sig_peptide

<222> 196..240

<223> Von Heijne matrix

score 6.69999980926514

seq ILSTVTALTFARA/LD

<221> polyA_signal

<222> 461..466

<221> polyA_site

<222> 485..496

<400> 335

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aaaaaattgg tcccagtttt caccctgccg cagggctggc tggggagggc agcggtttag      60
attagccgtg gcctaggccg tttaacgggg tgacacgagc htgcagggcc gagtccaagg      120
cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag      180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt      231
                Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
                -15                -10                -5
gcc aga gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt      279
Ala Arg Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
                1                5                10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag agc agc cac tcg      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser
                15                20                25
gcc cca gga tca acc cag cac cga aga aaa aca acc aga aga aat tat      375
Ala Pro Gly Ser Thr Gln His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
                30                35                40                45
tct tca gcc tgaaatgaak ccgggatcaa atgggttgctg atcaragccc      424
Ser Ser Ala
atattttaaat tggaaaagtc aaattgasca ttattaaata aagcttggtt aatatgtctc      484
aaacaaaaaa aa      496
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<210> 336

<211> 968

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 54..590

<221> sig_peptide

<222> 54..227

<223> Von Heijne matrix

score 3.5

seq GGILMGSFQGTIA/GQ

<221> polyA_site

<222> 955..965

<400> 336

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atatttgccc cttactttat cttgtgcctt gagaaattgc tggggagaga ggt atg      56
                Met
tcc act ggg cag ctg tac agg atg gag gat ata ggg cgt ttc cac tcc      104
Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser
                -55                -50                -45
cag cag cca ggt tcc ctc acc cca agc tca ccc act gtt ggg gag att      152
Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile
                -40                -35                -30
atc tac aat aac acc aga aac aca ttg ggg tgg att ggg ggt atc ctt      200
Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu
                -25                -20                -15                -10
```

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atg ggt tct ttt cag gga acc att gct gga caa ggc aca gga gcc acc      248
Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr
      -5                      1                      5
tcc att tct gag ctc tgc aag gga caa gaa cta gag cca tca ggg gct      296
Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala
      10                      15                      20
ggg ctc act gtg gcc cca ccc caa gcc gtc agc ctc cag ggw atc tac      344
Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ile Tyr
      25                      30                      35
acc ctg cct tgg ctg cta cag ctt ttt cac tcc act gcc cta rgg gna      392
Thr Leu Pro Trp Leu Leu Gln Leu Phe His Ser Thr Ala Leu Xaa Xaa
      40                      45                      50                      55
dtt cag caa cct aat gga tct cta tct ctg aac atc tct tca tcc cat      440
Xaa Gln Gln Pro Asn Gly Ser Leu Ser Leu Asn Ile Ser Ser Ser His
      60                      65                      70
gct ccr rgt cca rca acc tgc acc ctg gaa cca gga gtg gac cct acc      488
Ala Pro Xaa Pro Xaa Thr Cys Thr Leu Glu Pro Gly Val Asp Pro Thr
      75                      80                      85
cga sct gtc tgt att aat ccc cat ccc cca cca cca atc tta aaa abc      536
Arg Xaa Val Cys Ile Asn Pro His Pro Pro Pro Pro Ile Leu Lys Xaa
      90                      95                      100
cct ctg tcc ccc tac cct aaa ccc cag tta ggt acc cat gct ggg caa      584
Pro Leu Ser Pro Tyr Pro Lys Pro Gln Leu Gly Thr His Ala Gly Gln
      105                      110                      115
gtc aat taacaattta tgcacaggta ctagtattat tgtattaccg ttccagggta      640
Val Asn
120
gctttgaaaa aagtatctca aaaaggcaac atgggccgag cgcagtggct cacgcctgta      700
atcccagcac tttgggaggc caaggtgggc agatcgccctg aggtctggag ttcaagacca      760
gcctggccaa caggggtgaaa ccccgctctct acaaaaaatar gaaaatttrgc caggtgtggg      820
ggcagacgtc tgrgtccca gctattcagg agactgaggc acgagaattc catgaacca      880
ggatgcggag gttgcagtga gccgagattg tgccactgcg ctccagcctg ggcgacagag      940
tggtattctg tttcaaaaaa aaaaamcm                                968

<210> 337
<211> 901
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..846

<221> sig_peptide
<222> 133..345
<223> Von Heijne matrix
      score 9.39999961853027
      seq VVSFLLLLLAGLIA/TY

<221> polyA_site
<222> 890..901

<400> 337
aagcagcttc caggatcctg agatccggag cagccggggg cggagcggct cctcaagagt      60
tactgatcta tnnatggcag agaaaaaaaa attgtgacca gagacgtgta gcaatgaaca      120

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aggaacrtca ta atg rwn nnk ttc aca gac ccc tct tca gtg aat gaa aag 171
      Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
      -70          -65          -60
aag agg agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag 219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
      -55          -50          -45
ccg ctc att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg 267
Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu
      -40          -35          -30
aag gaa tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct 315
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser
      -25          -20          -15
ttt tta ctg ctg ctt gct ggg ctt ata gct acg tat tat gtt gaa gga 363
Phe Leu Leu Leu Leu Ala Gly Leu Ile Ala Thr Tyr Tyr Val Glu Gly
      -10          -5          1          5
gtg cat caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat 411
Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr
      10          15          20
gcc tac tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca 459
Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr
      25          30          35
ggg ctg cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt 507
Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val
      40          45          50
aca tta gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc 555
Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro
      55          60          65          70
tat cct gat cag att att tgt cca gat gaa gag ggc act gaa gga acc 603
Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr
      75          80          85
att tct ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg 651
Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met
      90          95          100
tgg ggt atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc 699
Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala
      105          110          115
aga gca gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag 747
Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln
      120          125          130
gaa ttt gaa gag atg ctg gaa cat gca gag tct gca caa gta aga aca 795
Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Val Arg Thr
      135          140          145          150
gtg ggg ata gaa aat aga aca ctt tac ttc ttc cta aag agg cta tta 843
Val Gly Ile Glu Asn Arg Thr Leu Tyr Phe Phe Leu Lys Arg Leu Leu
      155          160          165
agg taaaattggt agtagttact ctgaagaaga aaactgctaa agtaaaaaaa aaaaa 901
Arg

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<210> 338

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 138..671

<221> sig_peptide

<222> 138..248

<223> Von Heijne matrix

score 3.5

seq LVFNFLILITILT/IW

<221> polyA_signal

<222> 1319..1324

<221> polyA_site

<222> 1338..1347

<400> 338

aagaatgctt	gtgaagtagc	aactaaagtg	gcagtgtttc	ttctgaaatt	ctcaggcagt	60
cagactgtct	taggcaaadc	ttgataaaat	agcccttadc	caggttttta	tctaaggaat	120
cccaagaaga	ctggggga	atg gag aga	cag tca agg	gtt atg tca	gaa aag	170
		Met Glu Arg	Gln Ser Arg	Val Met Ser	Glu Lys	
		-35		-30		
gat gag tat	cag ttt caa	cat cag gga	gcg gtg gag	ctg ctt gtc	ttc	218
Asp Glu Tyr	Gln Phe Gln	His Gln Gly	Ala Val Glu	Leu Leu Val	Phe	
-25		-20		-15		
aat ttt ttg	ctc atc ctt	acc att ttg	aca atc tgg	tta ttt aaa	aat	266
Asn Phe Leu	Leu Ile Leu	Thr Ile Leu	Thr Ile Trp	Leu Phe Lys	Asn	
-10		-5		1	5	
cat cga ttc	cgc ttc ttg	cat gaa act	gga gga gca	atg gtg tat	ggc	314
His Arg Phe	Arg Phe Leu	His Glu Thr	Gly Gly Ala	Met Val Tyr	Gly	
	10		15		20	
ctt aya atg	gga cta att	tta csa tat	gct aca gca	cca act gat	att	362
Leu Xaa Met	Gly Leu Ile	Leu Xaa Tyr	Ala Thr Ala	Pro Thr Asp	Ile	
	25		30		35	
gaa agt ggr	rct gtc tat	gac tgt gta	aaa cta act	ttc agt cca	tca	410
Glu Ser Gly	Xaa Val Tyr	Asp Cys Val	Lys Leu Thr	Phe Ser Pro	Ser	
	40		45		50	
act ctg ctg	gtt aat atc	act gac caa	gtt tat gar	tat aaa tac	aar	458
Thr Leu Leu	Val Asn Ile	Thr Asp Gln	Val Tyr Glu	Tyr Lys Tyr	Lys	
55		60		65	70	
aga gaa ata	agt cag cac	amc atc aat	cct cat cam	gga aat gct	ata	506
Arg Glu Ile	Ser Gln His	Xaa Ile Asn	Pro His Xaa	Gly Asn Ala	Ile	
	75		80		85	
ctt gaa aag	atg aca ttt	gat cca raa	atc ttc ttc	aat gtt tta	ctg	554
Leu Glu Lys	Met Thr Phe	Asp Pro Xaa	Ile Phe Phe	Asn Val Leu	Leu	
	90		95		100	
cca cca att	ata ttt cat	gca gga tat	agt cta aag	aag aga cac	ttt	602
Pro Pro Ile	Ile Phe His	Ala Gly Tyr	Ser Leu Lys	Lys Arg His	Phe	
	105		110		115	
ttt caa aac	tta gga tct	att tta acg	tat gcc ttc	ttg gga act	gcc	650
Phe Gln Asn	Leu Gly Ser	Ile Leu Thr	Tyr Ala Phe	Leu Gly Thr	Ala	
	120		125		130	
atc tcc tgc	atc gtc ata	ggg taagt	gacat tcggag	ctca agttgc	caggt	701
Ile Ser Cys	Ile Val Ile	Gly				
135		140				
ggctgtgggg	tcygtgatct	gtgtgaggga	tctaacactt	ccaggattct	tgctggckgg	761
gaaaattgtc	ttttttttar	tawatcacaw	atttgtatgt	tttttcwgac	ttaattccac	821
ggcttckgam	aaatacaagg	cttcaaatca	aagcaaaacta	waggattgct	ggactttctc	881
tgtgagttct	ggactttctga	cttaggggaat	gtggatcact	tgcttgagt	tatgtgaagc	941

gcattgcatt	cttcttttag	tttgagtaat	sccgatatgc	tcactgcatt	cttttttgtc	1001
ttgtattgag	agaccttacc	tgtatttggc	aggagtgc	aaagtaactat	atgccaaagag	1061
ttttctttct	aaaggaaaagt	ttacaagaca	gcagtctgaa	acagatatgt	ccaaatatca	1121
acagagttgc	ttaatacagg	gatagctttt	cagttaatac	cctgtagaat	gcagactctt	1181
tttttcattg	tattttcttg	attatgctac	tgagccctaa	gtcacacgtt	atatactctg	1241
gcttgcagct	catcataaag	taaaatgtgg	taccaaatgg	tgaaggcaat	ccagcctctg	1301
ataatcccgt	ccaatacatt	aaagctccac	tcagggaaaa	aaaaaa		1347

<210> 339
 <211> 987
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..411

<221> sig_peptide
 <222> 124..186
 <223> Von Heijne matrix
 score 6.30000019073486
 seq MVALCCCLWKISG/CE

<221> polyA_signal
 <222> 948..953
 <221> polyA_site
 <222> 971..983

<400> 339	
aagacgctgc	cttttagggag agataaaaag cataatgaca ttagctagga aagttaattt 60
tcagttctta	ctgaagtgtc gtatgaaact gaaatttcca aggaactgaa ttttgtgagc 120
caa atg agc atg caa ttc ttg ttt aag atg gtg gcc tta tgc tgt tgt	168
Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys	
-20 -15 -10	
ctc tgg aag atc tcc ggc tgt gag gaa gtc cct cta act tac aac ctg	216
Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu	
-5 1 5 10	
ctc aag tgc ctc cta gat aaa gcg cac tgt gta ctc ctg aca cct tgt	264
Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys	
15 20 25	
ggt tac atc ttt tcc ttg atc agt cca gaa att ctc aaa ctc act tta	312
Gly Tyr Ile Phe Ser Leu Ile Ser Pro Glu Ile Leu Lys Leu Thr Leu	
30 35 40	
atc act ttg cav atc ctc tta ata ctc aaa aat cta cac tta ctg tgg	360
Ile Thr Leu Xaa Ile Leu Leu Ile Leu Lys Asn Leu His Leu Leu Trp	
45 50 55	
ctg aca gtt tca agc awa tgt gtt cat cgc agt agt gca aga aaa gaa	408
Leu Thr Val Ser Ser Xaa Cys Val His Arg Ser Ser Ala Arg Lys Glu	
60 65 70	
aag tagaagaacc ctgcagagat ttgatggaac ccagcttcta ttcattaaaa	461
Lys	
75	
ccaatggcaa aatataaagc aaataggagg tgacgaagggt tacaaaaata cgtattgttt	521
atgttttccc tgggggtgtgc tgattgtcag gcatcagttc cctgtgccat tcattcccca	581

acacagcatg	catcagaaat	tttatcaata	aatgctttct	ctctcaatgt	tcaacctatg	641
ctgatatgacc	attaaatata	gtttttgggt	tcacagcttg	tcacatcat	ttgtctatac	701
ctgtggcaaa	gaatatctaa	taagatactc	tcagcatttt	gcacacttaa	actaagatgc	761
tgaatgctgt	attttacgga	ataatcagcc	acattaaatt	tggagactca	acaagcatgc	821
tgtgaacatt	caacattagg	tttaaatttt	atttttaaaa	gttaataata	aaaggatata	881
tgtaagtat	tatgaaaccc	tgcatatact	gtaataaaat	ggtggatgtg	aatggacaat	941
atatgcaata	aaatttataa	tttgattcya	aaaaaaaaaa	aamccv		987

<210> 340
<211> 748
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 372..494

<221> sig_peptide
<222> 372..443
<223> Von Heijne matrix
score 5.30000019073486
seq RILLLHFYCLLRS/SE

<221> polyA_signal
<222> 708..713

<221> polyA_site
<222> 732..745

<400> 340						
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tgaggttgtg	taattcagct	ggccctggct	cctggtccct	gttactgagc	tgggcagtcg	120
gaaccgaaggc	agatgagctc	aagatcatgc	cttgggaagc	atggtgctct	aggggtgcct	180
ttttattcct	ttcattgtat	tatagactgt	ttccaagttt	atggttagaa	atggtaaagt	240
gggtctgggtg	ttttgaggta	gaacccagcc	tagggcaaga	tatgaactgt	tcttgaggta	300
gaaatgtcta	cagtcagttg	tttcatctag	cttgcacatt	aaaacacaaa	cccttcagtt	360
gctttcactt	a atg cac aca ttt gcc	aat gac aga ggg	tta tac agg atc			410

Met His Thr Phe Ala Asn Asp Arg Gly Leu Tyr Arg Ile

-20 -15

ctt ctt tta cat ttc tat tgt ctg cta cgc tca tca gag tat att ttg	458
Leu Leu Leu His Phe Tyr Cys Leu Leu Arg Ser Ser Glu Tyr Ile Leu	
-10 -5 1 5	

ggg tac aag gtt ttg ggg gtt ttt tty ccc att ttg taactgcctt	504
Gly Tyr Lys Val Leu Gly Val Phe Phe Pro Ile Leu	

10 15

attgaaaadt	aaktgccctt	ccattccagg	cctcctcata	ttgtacttgt	ttcctgccaa	564
atctggggga	tcatattgtat	tttaactttg	taatctatgg	ctctgtactg	ttgaaagstc	624
tcaattctgt	ggggtctcct	tagtatgtat	gtgacttttc	atgttgcaat	atcacacgat	684
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accc						748

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<212> DNA

<213> Homo sapiens

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<222> 112..450

<221> sig_peptide

<222> 112..192

<223> Von Heijne matrix

score 7.19999980926514

seq SLLFFLLLEGGXT/EQ

<221> polyA_signal

<222> 1053..1058

<221> polyA_site

<222> 1095..1106

<400> 341

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gaaggcvakk rcnnnnrctt gaaggttctg tcaccttttg cagtgggtcca a atg aga	117
	Met Arg
raa aag tgg aaa atg gga ggc atg aaa tac atc ttt tcg ttg ttg ttc	165
Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe	
-25 -20 -15 -10	
ttt ctt ttg cta gaa gga ggc kaa aca gag caa gtr amn cat tca gag	213
Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu	
-5 1 5	
aca tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg	261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp	
10 15 20	
cat cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc	309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile	
25 30 35	
atgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat	357
Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn	
40 45 50 55	
gtt cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc	405
Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg	
60 65 70	
tgc cca gaa gac tcc tta ccc cca gtg aac aat rwg gtg acc agc	450
Cys Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Xaa Val Thr Ser	
75 80 85	
tagtcttgck agtacaatgg gacaacttac caacatggas agctgttcgt agctgrrggg	510
ctctttcaga atcggcaacc cmatcaatgc acccagtgca gctgttcgga rggaaacktg	570
tattgtggtc tcaagacttg ccccaaatta acctgtgcct tcccagtcct tgttccarat	630
tcctgctgcc gggwtgacag argagatgga caactgtcat gggaacmttc tgatggtgat	690
atcttcgggc aacctgccaa cagagaagca agacattctt accaccgctc tcactatgat	750
cctccaccaa gccgacaggc tggaggtctg tcccgccttc ctggggccag aagtcaccgg	810
ggagctctta tggattccca gcaagcatca ggaaccattg tgcaaattgt catcaataac	870
aaacacaagc atggacaagt gtgtgtttcc aatggaaaga cctattctca tggcgagtcc	930
tggcacccaa acctccgggc atttggcatt gtggagtgtg tgctatgtac ttgtaatgtc	990
accaagcaag agtgaagaa aatccactgc cccaatcgat acccctgcaa gtatcctcaa	1050
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 <213> Homo sapiens

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 <222> 117..170
 <223> Von Heijne matrix
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 seq LILLALATGLVGG/ET

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 <222> 1159..1164

<221> polyA_site
 <222> 1178..1190

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 Met
 agg att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg 167
 Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly
 -15 -10 -5
 gga gag acc agg atc atc aag ggg ttc gag tgc aag cct cac tcc cag 215
 Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
 1 5 10 15
 ccc tgg cag gca gcc ctg ttc gag aag acg cgg cta ctc tgt ggg gcg 263
 Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
 20 25 30
 acg ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag 311
 Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
 35 40 45
 ccc cgc tac ata ktt cac ctg ggg cag cac aac ctc cag aag gag gag 359
 Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu Glu
 50 55 60
 ggc tgt gag car acc cgg aca gcc act gag tcc ttc ccc cac ccc ggc 407
 Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly
 65 70 75
 ttc aac aac agc ctc ccc aac aaa gac cam mgc aat gac atc atg ctg 455
 Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met Leu
 80 85 90 95
 gtg aak atg gma tgc cca gtc tcc atc acc tgg gct gtg cga ccc ctc 503
 Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu
 100 105 110
 acc ctc tcc tca cgc tgt gtc act gct ggc acc agc tgc ctc att tcc 551
 Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile Ser
 115 120 125
 ggc tgg ggc agc acg tcc agc ccc cag tta cgc ctg cct cac acc ttg 599
 Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu
 130 135 140
 cga tgc gcc aac atc acc atc att gag cac cag aag tgt gag aac gcc 647

cg	g	c	a	c	a	g	a	a	t	g	t	c	g	c	g	a	t	t	g	c	t	t	c	t	c	t		195		
Arg	Gly	Leu	Leu	His	Ser	Ser	Lys	Trp	Ser	Ala	Glu	Leu	Ala	Phe	Ser															
25					30				35					40																
c	t	c	c	t	g	c	a	t	t	g	c	c	t	g	c	c	a	a	c	c	c	c	c	a	t	t	a	c	a	243
Leu	Pro	Ala	Leu	Pro	Leu	Ala	Glu	Leu	Gln	Pro	Pro	Pro	Pro	Ile	Thr															
				45				50					55																	
g	a	g	a	a	g	a	a	g	a	a	g	a	a	g	a	a	g	a	a	g	a	a	g	a	a	g	a	a	291	
Glu	Glu	Asp	Ala	Gln	Asp	Met	Asp	Ala	Tyr	Thr	Leu	Ala	Lys	Ala	Tyr															
			60				65					70																		
t	t	t	g	a	c	g	t	t	a	a	a	g	a	g	a	t	a	t	a	a	g	a	g	a	t	a	a	g	a	339
Phe	Asp	Val	Lys	Glu	Tyr	Asp	Arg	Ala	Ala	His	Phe	Leu	His	Gly	Cys															
			75				80					85																		
a	a	t	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	387	
Asn	Ala	Arg	Lys	Ala	Tyr	Phe	Leu	Tyr	Met	Tyr	Ser	Arg	Tyr	Leu	Val															
			90				95					100																		
a	g	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	435	
Arg	Ala	Ile	Leu	Lys	Cys	His	Ser	Ala	Phe	Ser	Glu	Thr	Ser	Ile	Phe															
			105				110					115																		
a	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	485	
Arg	Thr	Asn	Gly	Lys	Val	Lys	Ser	Phe	Lys																					
			125				130																							
g	a	a	t	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	545	
a	g	a	t	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	605	
a	t	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	665	
g	a	a	t	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	725	
a	g	t	a	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	785	
a	g	t	a	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	845	
a	t	t	a	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	905	
a	c	a	t	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	t	a	t	965	
g	a	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1025	
a	c	t	g	g	t	t	g	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1070	

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 <212> DNA
 <213> Homo sapiens

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 <222> 2..718
 <221> sig_peptide
 <222> 2..76
 <223> Von Heijne matrix
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 seq RVGLLLGGGGVYG/SR

<221> polyA_signal
 <222> 1170..1175

<221> polyA_site
 <222> 1203..1213

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tta	ctc	ggt	ggt	ggc	gga	gtc	tac	gga	agc	cgt	ttt	cgc	ttc	act	ttt	97
Leu	Leu	Gly	Gly	Gly	Gly	Val	Tyr	Gly	Ser	Arg	Phe	Arg	Phe	Thr	Phe	
				-5				1				5				
cct	ggc	tgt	aga	gcg	ctt	tcc	ccc	tgg	cgg	gtg	aga	vtg	cag	aga	cga	145
Pro	Gly	Cys	Arg	Ala	Leu	Ser	Pro	Trp	Arg	Val	Arg	Xaa	Gln	Arg	Arg	
	10					15					20					
agg	tgc	gag	atg	agc	act	atg	ttc	gcg	gac	act	ctc	ctc	atc	gtt	ttt	193
Arg	Cys	Glu	Met	Ser	Thr	Met	Phe	Ala	Asp	Thr	Leu	Leu	Ile	Val	Phe	
	25					30					35					
atc	tct	gtg	tgc	acg	gct	ctg	ctc	gca	gag	ggc	ata	acc	tgg	gtc	ctg	241
Ile	Ser	Val	Cys	Thr	Ala	Leu	Leu	Ala	Glu	Gly	Ile	Thr	Trp	Val	Leu	
	40				45					50					55	
gtt	tac	agg	aca	gac	aag	tac	aag	aga	ctg	aag	gca	gaa	gtg	gaa	aaa	289
Val	Tyr	Arg	Thr	Asp	Lys	Tyr	Lys	Arg	Leu	Lys	Ala	Glu	Val	Glu	Lys	
				60					65					70		
cag	agt	aaa	aaa	ttg	gaa	aag	aag	aag	gaa	aca	ata	aca	gag	tca	gct	337
Gln	Ser	Lys	Lys	Leu	Glu	Lys	Lys	Lys	Glu	Thr	Ile	Thr	Glu	Ser	Ala	
				75				80					85			
ggt	cga	caa	cag	aaa	aar	aaa	ata	gag	aga	cdd	kaa	kas	amc	ctg	arg	385
Gly	Arg	Gln	Gln	Lys	Lys	Lys	Ile	Glu	Arg	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	
				90			95					100				
aat	aac	aac	aga	gat	cta	tca	atg	gtt	cga	atg	aaa	tcc	atg	ttt	gct	433
Asn	Asn	Asn	Arg	Asp	Leu	Ser	Met	Val	Arg	Met	Lys	Ser	Met	Phe	Ala	
	105					110					115					
att	ggc	ttt	tgt	ttt	act	gcc	cta	atg	gga	atg	ttc	aat	tcc	ata	ttt	481
Ile	Gly	Phe	Cys	Phe	Thr	Ala	Leu	Met	Gly	Met	Phe	Asn	Ser	Ile	Phe	
	120					125					130				135	
gat	ggt	aga	gtg	gtg	gca	aag	ctt	cct	ttt	acc	cct	ctt	tct	tas	rtc	529
Asp	Gly	Arg	Val	Val	Ala	Lys	Leu	Pro	Phe	Thr	Pro	Leu	Ser	Xaa	Xaa	
				140						145				150		
sra	gga	ctg	tct	cat	cga	aat	ctg	ctg	gga	gat	gac	acc	aca	gac	tgt	577
Xaa	Gly	Leu	Ser	His	Arg	Asn	Leu	Leu	Gly	Asp	Asp	Thr	Thr	Asp	Cys	
				155					160					165		
tcc	ttc	att	ttc	ctg	taw	att	ctc	tgt	act	atg	tcg	att	cga	cag	aac	625
Ser	Phe	Ile	Phe	Leu	Xaa	Ile	Leu	Cys	Thr	Met	Ser	Ile	Arg	Gln	Asn	
				170			175						180			
att	cag	aag	att	ctc	ggc	ctt	gcc	cct	tca	cga	gcc	gcc	acc	aag	cag	673
Ile	Gln	Lys	Ile	Leu	Gly	Leu	Ala	Pro	Ser	Arg	Ala	Ala	Thr	Lys	Gln	
				185			190					195				
gca	ggt	gga	ttt	ctt	ggc	cca	cca	cct	cct	tct	ggg	aag	ttc	tct		718
Ala	Gly	Gly	Phe	Leu	Gly	Pro	Pro	Pro	Pro	Ser	Gly	Lys	Phe	Ser		
	200				205					210						
tgaactcaag	aactctttat	tttctakcat	tctttctaga	cacacacaca	tcagactggc											778
aactgttttg	tascaagagc	cataggtagc	cttackactt	gggcctcttt	ctagtgttg											838
attattttcta	agccttttgg	gtatkattag	agtgaataatg	gcagccagca	aacttgatag											898
tgcttttggt	cctagatgat	ttttatcaaa	taagtggatt	gattagttaa	gttcaggtaa											958
tgtttatgta	atgaaaaaca	aatagcatcc	ttcttggttc	atttacataa	gtattttctg											1018
tgggaccgac	tctcaaggca	ctgtgtatgc	cctgcaagtt	ggctgtctat	gagcatttag											1078
agatttagaa	gaaaaattta	gtttgtttta	cccttgtaac	tgtttgtttt	gttggtgttt											1138
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<211> 978
<212> DNA
<213> Homo sapiens

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<222> 86..709

<221> sig_peptide
<222> 86..361
<223> Von Heijne matrix
score 6.30000019073486
seq LLMSILALIFIMG/NS

<221> polyA_signal
<222> 943..948

<221> polyA_site
<222> 963..973

<400> 345

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ggacgaaaga gtcggcgccg ccgta atg cga gag ccg cag aag aga acc gca	112
Met Arg Glu Pro Gln Lys Arg Thr Ala	
-90 -85	
aca atc gca aaa tyc rrg gcs tva gag ggc ctc cga gac ccc tat ggc	160
Thr Ile Ala Lys Xaa Xaa Ala Xaa Glu Gly Leu Arg Asp Pro Tyr Gly	
-80 -75 -70	
cgc ctc tgt ggt agc gag cac ccc cga aga cca cct gag cgg ccc gag	208
Arg Leu Cys Gly Ser Glu His Pro Arg Arg Pro Pro Glu Arg Pro Glu	
-65 -60 -55	
gaa gac ccg agc act cca gag gag gcc tct acc acc cct gaa gaa gcc	256
Glu Asp Pro Ser Thr Pro Glu Glu Ala Ser Thr Thr Pro Glu Glu Ala	
-50 -45 -40	
tcg agc act gcc caa gca caa aag cct tca gtg ccc cgg agc aat ttt	304
Ser Ser Thr Ala Gln Ala Gln Lys Pro Ser Val Pro Arg Ser Asn Phe	
-35 -30 -25 -20	
cag ggc acc aag aaa agt ctc ctg atg tct ata tta gcg ctc atc ttc	352
Gln Gly Thr Lys Lys Ser Leu Leu Met Ser Ile Leu Ala Leu Ile Phe	
-15 -10 -5	
atc atg ggc aac agc gcc aag gaa gct ctg gtc tgg aaa gtg ctg ggg	400
Ile Met Gly Asn Ser Ala Lys Glu Ala Leu Val Trp Lys Val Leu Gly	
1 5 10	
aag tta gga atg cag cct gga cgt cas cac agc atc ttt gga gat ccg	448
Lys Leu Gly Met Gln Pro Gly Arg Xaa His Ser Ile Phe Gly Asp Pro	
15 20 25	
aag aar atc gtc aca gaa ran ttt gtg cgc aga ggg tac ctg att tat	496
Lys Lys Ile Val Thr Glu Xaa Phe Val Arg Arg Gly Tyr Leu Ile Tyr	
30 35 40 45	
ara ccg gtg ccc cgt abc agt ccg gtg gag tat gas ttc ttc tgg ggg	544
Xaa Pro Val Pro Arg Xaa Ser Pro Val Glu Tyr Xaa Phe Phe Trp Gly	
50 55 60	
ccc cga gca cac gtg gaa tcg agc ara ctg aaa stc wtg cat ttt gtg	592
Pro Arg Ala His Val Glu Ser Ser Xaa Leu Lys Xaa Xaa His Phe Val	
65 70 75	
gca agg gtt cgt aac cga tgc tct aaa gac tgg cct tgt aat tat gac	640
Ala Arg Val Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp	

80	85	90	
tgg gat tcg gac gat gat gca gag gtt gag gct atc ctc aat tca ggt			688
Trp Asp Ser Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly			
95	100	105	
gct arg ggt tat tcc gcc cct taagtaratc tgaggcagac ccttgggggt			739
Ala Xaa Gly Tyr Ser Ala Pro			
110	115		
gtaaaagaga gtcacaggta ccccaaggag tagatgccag ggtcctaagt tgaaaatgmt			799
gtcgattggg ggcgggggac actgtatttg atatttgtga tcagtgatca ttgttcaact			859
gcgaaataga gtgtttgctt ttgataatgg aaaattgtat tcgtttttaa attccgtttg			919
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<210> 346
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 63..320

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 <222> 63..179
 <223> Von Heijne matrix
 score 3.90000009536743
 seq VLAIGLLHIVLLS/IP

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 <222> 771..776

<221> polyA_site
 <222> 799..810

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gg atg aat gtk ggc aca gcg cac ags dag gtg aac ccc aac acg cgg	107
Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg	
-35 -30 -25	
gtk atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt	155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly	
-20 -15 -10	
ctc ctc cac atc gtg ctg ctg agc atc ccg ttt gtk agt gtc cct gtc	203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val	
-5 1 5	
gtc tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc	251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe	
10 15 20	
ctg cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag	299
Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys	
25 30 35 40	
gcg agg ctg cta acc cac tgg tgagcagatg gattatgggg tccagttcac	350
Ala Arg Leu Leu Thr His Trp	
45	
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cactaaktac raccaaatac attttgtgct caacaccgtg tccctgatra gcgtgcttat	470

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cascccccttc	ccctgcccag	ggtggcaggg	gaggggtagg	gtaaaaggca	tktgctgcaa	590
chctgaaaaac	araaaraara	rscctctgga	cactgccara	ratggggggt	gagcctctgg	650
cctaattttcc	cccctcgctt	cccccagtag	ccaacttgga	gtagcttgta	ytgggggttg	710
ggtagggcccc	ctggggtctg	accttttctg	aattttttga	tcttttcctt	ttgctttttg	770
aatararact	ccatggagtt	ggtcatggaa	aaaaaaaaaa			810

<210> 347
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 <212> DNA
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 <222> 299..418

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 <223> Von Heijne matrix
 score 3.59999990463257
 seq LLLLLITPSPSPL/LF

<221> polyA_signal
 <222> 739..744

<221> polyA_site
 <222> 762..771

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aaatgatgtc	catttgagcc	ccaccacgga ggttatgtgg tccccaaaagg aatgatggcc 180
aagcaattaa	tttttcctcc	tagttcttag cttgcttctg cattgattgg ctttacacaa 240
ctggcattta	gtctgcatta	cacaaataga cactaattta tttggaacaa gcagcaaa 298
atg aga act	tta ttt ggt	gca gtc agg gct cca ttt agt tcc ctc act 346
Met Arg Thr	Leu Phe Gly	Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
	-25	-20 -15
ctg ctt cta	atc acc cct	tct ccc agc cct ctt cta ttt gat aga ggt 394
Leu Leu Leu	Ile Thr Pro	Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
	-10	-5 1 5
ctg tcc ctc	aga tca gca	atg tct tagccccctct cctctcttcc attccttcct 448
Leu Ser Leu	Arg Ser Ala	Met Ser
	10	
gttgggtactc	atttcttcta	actttttaata aacatttagg tataatacat tacagtaagt 508
gctattttaga	tacaaactta	aaacatacta tatattttaa ggatctaaga atcctttara 568
rrrggcacat	gactgaagta	cctcagctgc gcagcctgta accagttttt ttaatgtaaa 628
agtaaraatg	ccagccttaa	cctabccctg carataaaaag ctaactttta ttaataccag 688
ccctgaataa	tggcactaat	ccacactctt ccttaragtg atgctggaaa aataaaatca 748
ggggcttcag	attaaaaaaaa	aaa 771

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 <211> 409
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 186..380

<221> sig_peptide

<222> 186..233

<223> Von Heijne matrix

score 4

seq FFLFLSFVLMYDG/LR

<221> polyA_signal

<222> 383..388

<221> polyA_site

<222> 396..409

<400> 348

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acctagtttt ttaaagggtt gaataataa atgcagtatt tgcagtataa aaaggaagga 120

atttgtagag aatcattttg gtgctcaagt ctcttagcag tgccttattg cctcatagca 180

agaag atg ctg ggg ttt ttt ttg ttt ttg tcc ttt gta tta atg tat gat 230

Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp

-15

-10

-5

ggg ttg cgc ctt ttt ggc att ctt tca aca tgt cgt gta cat cac acc 278

Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr

1

5

10

15

atg aat cag ttc cta att gat ata tct agc ttt acc tcc cga gtt aaa 326

Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Lys

20

25

30

aaa aaa atc ttt tta ttt tat gcc ttc awa ggt tgc ycg ttt car agt 374

Lys Lys Ile Phe Leu Phe Tyr Ala Phe Xaa Gly Cys Xaa Phe Gln Ser

35

40

45

gcc aca taaataaaaat gtttaacaaa aaaaaaaaaa 409

Ala Thr

<210> 349

<211> 613

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 69..458

<221> sig_peptide

<222> 69..233

<223> Von Heijne matrix

score 4

seq AALCGISLSQLFP/EP

<221> polyA_signal

<222> 564..569

<221> polyA_site
<222> 602..613

<400> 349

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cgctggga atg gcc atg tgg aac agg cca tgb bag ang ctg cct cag cag      110
      Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
      -55                    -50                    -45
cct cts sta gct gag ccc act gca gag ggg gag cca cac ctg ccc acg      158
Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr
      -40                    -35                    -30
ggc cgg gas byg act gag gcc aac cgc ttc gcc tat gct gcc ctc tgt      206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
      -25                    -20                    -15                    -10
ggc atc tcc ctg tcc cag tta ttt cct gaa ccc gaa cac agc tcc ttc      254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
      -5                    1                    5
tgc aca gag ttc atg gca ggc ctg gtg ckm tgg ctg gag ttg tct gaa      302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
      10                    15                    20
gct gtc ttg cca acc atg act gct ttt gcg agc ggc ctg gga ggt gaa      350
Ala Val Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu
      25                    30                    35
gga sca vma tgt gtt tgt tca aat ttt act gaa gga ccc cat ctt gaa      398
Gly Xaa Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu
      40                    45                    50                    55
gga cga ccc gac ggt gat cac tca gga cct tct gag ctt ctc act caa      446
Gly Arg Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln
      60                    65                    70
gga tgg gca cta tgacscgg gccagagtc tcgtttgcc catgacctcc      498
Gly Trp Ala Leu
      75
ctgctccaag tgcccttgga ggagctggat gtccttgaaa agatgttcct ggagagcctg      558
aaggaaatca aagaagagga atctgaaatg gccgaggcat ccraaaaaaa aaaaa      613

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<210> 350

<211> 986

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 12..638

<221> sig_peptide

<222> 12..263

<223> Von Heijne matrix

score 4.19999980926514

seq ITMLQMLALLGYG/LF

<221> polyA_signal

<222> 951..956

<221> polyA_site

<222> 975..985

<400> 350

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                                -80                                -75
gga cct ctc atg ctg gtc ttc act ctg gtt gct atc cta ctc cat ggg      98
Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly
      -70                                -65                                -60
atg aag acg tct gac act att atc cgg gag ggc acc ctg atg ggc aca      146
Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr
      -55                                -50                                -45                                -40
gcc att ggc acc tgc ttc ggc tac tgg ctg gga gtc tca tcc ttc att      194
Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile
                                -35                                -30                                -25
tac ttc ctt gcc tac ctg tgc aac gcc cag atc acc atg ctg cag atg      242
Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met
                                -20                                -15                                -10
ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat tgc att gtc ctg ttc      290
Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe
      -5                                1                                5
atc acc tat aat atc cac ctc cgc gcc ctc ttc tac ctc ttc tgg ctg      338
Ile Thr Tyr Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu
      10                                15                                20                                25
ttg gtg ggt gga ctg tcc aca ctg cgc atg gta gca gtg ttg gtg tct      386
Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser
                                30                                35                                40
cgg acc gtg ggc ccc aca cad cgg mtg ctc ctc tgt ggc acc ctg gct      434
Arg Thr Val Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala
                                45                                50                                55
gcc cta cac atg ctc ttc ctg ctc tat ctg cat ttt gcc tac cac aaa      482
Ala Leu His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys
                                60                                65                                70
dtg gta dag ggg atc ctg gac aca ctg gag ggc ccc aac atc ccg ccc      530
Xaa Val Xaa Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro
      75                                80                                85
atc cag agg gtc ccc aga gac atc cct gcc atg ctc cct gct gct cgg      578
Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg
      90                                95                                100                                105
ctt ccc acc acc gtc ctc aac gcc aca gcc aaa gct gtt gcg gtg acc      626
Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr
                                110                                115                                120
ctg cag tca cac tgacccccacc tgaaattctt ggccagtcct ctttcccgca      678
Leu Gln Ser His
                                125
gctgcagaga ggargaasac tattaaagga cagtcctgat gacatgtttc gtagatgggg      738
tttgcagctg ccactgagct gtagctgcgt aagtacctcc ttgatgcctg tcggcacttc      798
tgaaaggcac aaggccaaga actcctggcc aggactgcaa ggctctgcag ccaatgcaga      858
aaatgggtca gtcctttga gaacccctcc ccacctaccc cttccttcct ctttatctct      918
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aaaaaaat                                                                986

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<210> 351

<211> 1447

<212> DNA

<213> Homo sapiens

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<222> 282..389

<221> sig_peptide
<222> 282..332
<223> Von Heijne matrix
score 3.5
seq RWWCFHLQAEASA/HP

<221> polyA_signal
<222> 1413..1418

<221> polyA_site
<222> 1437..1447

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gaagagctgt ggaggccacc ctctacaaag ctttatagaa cttctggatc taactcacia 180
acaagcttcc agaagagact agagacctta ggccaggaga tgaaggagt cagtagcaaa 240
gtcacacctg tccaattccc tgagctttgc tcaactcagct a atg gga tgg caa agg 296
Met Gly Trp Gln Arg
-15
tgg tgg tgc ttt cat ctt cag gca gaa gcc tct gcc cat ccc cct caa 344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
-10 -5 1
ggg ctg cag gcc caa ttc tca tgc tgc cct tgg gtg ggc atc tgt 389
Gly Leu Gln Ala Gln Phe Ser Cys Cys Pro Trp Val Gly Ile Cys
5 10 15
taacaaadga aaacgtctgg gtggcggcag cacttttgct ctgagtgcct acaaagctaa 449
tgcttggtgc tagaaacatc atcattatta aacttcagaa aagcagcagc catgttcagt 509
caggctcatg ctgcctcact gcttaagtgc ctgcaggagc cgcttgccaa rctccccctc 569
ctacacctgg cactctgggg tctgcacaag gctttgtcaa ccaaacacag cttccccccw 629
ttgattgcct gtagactttg gagccaaraa aactctgtg tgactctaca cacacttcag 689
gtgggtttgtg cttcaaagtc attgatgcaa cttgaaagga aacagtttaa tgggtggaaat 749
gaattaccat ttataacttc tgttttttta ttgagaaaat gattcacgaa kkccaaatca 809
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<210> 352
<211> 1641
<212> DNA
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<222> 208..339

<221> sig_peptide
<222> 208..294
<223> Von Heijne matrix
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seq LFLQLLVSH EIVC/AT

<221> polyA_site
<222> 1631..1641

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gcaagcttac caaggaggag atcgttgaca agtatgactt atttgttggc agccaggcca 180
cagattttgg ggaggcctta gtacggc atg atg agt tct gag cta cgg agg aac 234
Met Met Ser Ser Glu Leu Arg Arg Asn
-25
cct cat ttc ctc aaa agt aat tta ttt tta cag ctt ctg gtt tca cat 282
Pro His Phe Leu Lys Ser Asn Leu Phe Leu Gln Leu Leu Val Ser His
-20 -15 -10 -5
gaa att gtt tgc gct act gag act gtt act aca aac ttt tta aga cat 330
Glu Ile Val Cys Ala Thr Glu Thr Val Thr Thr Asn Phe Leu Arg His
1 5 10
gaa aag gcg taatgaaaac catcccgtcc ccattcctcc tcctctctga 379
Glu Lys Ala
15
gggactggag ggaagccgtg cttctgagga acaactctaa ttagtacact tgtgttttga 439
ratttacacw wtgtattatg tattaacatg gcgtgtttat ttttgtattt ttctctggtt 499
gggagtatka tatgaaggat caaratcctc aactcacaca tgtaracaaa cattasctct 559
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aa 1641

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<212> DNA

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<221> CDS

<222> 69..557

<221> sig_peptide

<222> 69..224

<223> Von Heijne matrix

score 4.69999980926514

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<221> polyA_signal

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<221> polyA_site

<222> 870..883

<400> 353

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Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala	
-50 -45 -40	
Cct tcc cca atg ccc cag cta cct cct gat acc ctt gag atg cgg gtc	158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val	
-35 -30 -25	
cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct ctg ggt cgg	206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg	
-20 -15 -10	
ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt tct ggc agg	254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg	
-5 1 5 10	
gct gca gga aag gct gtc agc tgc gct gag att gtc aag cgg cgg gtc	302
Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val	
15 20 25	
ccg ggc ctg cac cag ctc acc aag cta ckt ttc ctt caa act gag gac	350
Pro Gly Leu His Gln Leu Thr Lys Leu Xaa Phe Leu Gln Thr Glu Asp	
30 35 40	
agc tgg gtc cca scc tca cct gac aca ggg cta rac ccc ctc aca gtg	398
Ser Trp Val Pro Xaa Ser Pro Asp Thr Gly Leu Xaa Pro Leu Thr Val	
45 50 55	
cgc cgc cat gtg cct gca ktg tgg gtg ctg ctc asc cgg gac ccc ctg	446
Arg Arg His Val Pro Ala Xaa Trp Val Leu Leu Xaa Arg Asp Pro Leu	
60 65 70	
gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc cct ggc ctg	494
Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu	
75 80 85 90	
ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cra aaa agg gct	542
Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Xaa Lys Arg Ala	
95 100 105	
cra rac acc cga tcg tgaaaaacctg ctgasccagc ctgtttctccg ggcctraatg	597
Xaa Xaa Thr Arg Ser	
110	
tctgggggtgc ttgtgccttt tctranaagc gttgtgaskg ctcaacatcc ccatcaagggt	657
ttgagtcacac aaaagtggac ctccctatca tgcttccccct tccctctagc atgtgggaag	717
ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt gctaaataag	777
ggcttcctct gccttctacc tacagtgcac ttgaactgcc ttctgaaaga ggtccakgga	837

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884

<210> 354

<211> 729

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 134..325

<221> sig_peptide

<222> 134..274

<223> Von Heijne matrix

score 5.90000009536743

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<221> polyA_site

<222> 718..729

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tgaaagavat tct atg cat ggt ttt gaa ata ata tcc ttg aaa gag gaa 169

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu

-45

-40

tca cca tta gga aag gtg agt cag ggt cct ttg ttt aat gtg act agt 217

Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser

-35 -30 -25 -20

ggc tca tca tca cca gtg acc tgg ttg ggc cta ctc tcc ttc cag aac 265

Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn

-15

-10

-5

ctg cat tgc ttc cca gac ctc ccc act gag atg cct cta ara gcc aaa 313

Leu His Cys Phe Pro Asp Leu Pro Thr Glu Met Pro Leu Xaa Ala Lys

1

5

10

ggg ktc aac act tgagcctagg gtgggctaca acaaaaaratt ctaattttacc 365

Gly Xaa Asn Thr

15

ttgcttcac taggtccagg ccccaaktag cttgctgaag gaacttaaaa agtagctgtt 425

atattattgta ttgtataasc taaaaacatt tattttttgtt gaatcraaac aattccatgt 485

ascaatcttt tttctgttca cgggtgtttgt gataaaacct taaattccgc aagcatcagt 545

tttttgaaaa aatgggaatt gaccggatag wwacaggcaa agwtataaat agctacaaca 605

tcatttaact tttataaaca tgccttctct ctattgaara catctgatat ttttgctgga 665

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aaaa 729

<210> 355

<211> 1013

<212> DNA

<213> Homo sapiens

<220>

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<222> 78..731

<221> sig_peptide

<222> 78..227

<223> Von Heijne matrix
score 5.09999990463257
seq RTALILAVCCGSA/SI

<221> polyA_site

<222> 1002..1013

<400> 355

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                Met His His Gly Leu Thr Pro Leu Leu Leu Gly
                -50                -45                -40
gta cat gag caa aaa cag caa gtg gtg aaa ttt tta atc aag aaa aaa      158
Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys
                -35                -30                -25
gca aat tta aat gca ctg gat aga tat gga aga act gct ctc ata ctt      206
Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu
                -20                -15                -10
gct gta tgt tgt gga tcg gca agt ata gtc agc ctt cta ctt gag caa      254
Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
                -5                1                5
aac att gat gta tct tct caa gat cta tct gga cag acg gcc aaa aag      302
Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Lys Lys
                10                15                20                25
tat gct gtt tct agt cgt cat aat gta att tgc cag tta ctt tct gac      350
Tyr Ala Val Ser Ser Arg His Asn Val Ile Cys Gln Leu Leu Ser Asp
                30                35                40
tac aaa raa aaa cag atr cta aaa gtc tct tct gaa aac agc aat cca      398
Tyr Lys Xaa Lys Gln Xaa Leu Lys Val Ser Ser Glu Asn Ser Asn Pro
                45                50                55
raa caa gac tta aag ctg aca tca gag gaa gag tca caa agg ctt aaa      446
Xaa Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys
                60                65                70
gga agt gaa aat agc cag cca gag gaa atg tct caa gaa cca gaa ata      494
Gly Ser Glu Asn Ser Gln Pro Glu Glu Met Ser Gln Glu Pro Glu Ile
                75                80                85
aat arg ggt ggt gat aga aag gtt gaa raa raa atg aar aag cac gga      542
Asn Xaa Gly Gly Asp Arg Lys Val Glu Xaa Xaa Met Lys Lys His Gly
                90                95                100                105
agt wct cat atg gga ttc cca raa aac ctg mct aac ggt gcc act gct      590
Ser Xaa His Met Gly Phe Pro Xaa Asn Leu Xaa Asn Gly Ala Thr Ala
                110                115                120
gac aat ggt gat gat gga tta att ccm cca rgg aaa asc ara aca cct      638
Asp Asn Gly Asp Asp Gly Leu Ile Pro Pro Xaa Lys Xaa Xaa Thr Pro
                125                130                135
gaa agc cas caa ttt cct gac act gag aat gaa cag tat cac agg gac      686
Glu Ser Xaa Gln Phe Pro Asp Thr Glu Asn Glu Gln Tyr His Arg Asp
                140                145                150
ttt tct ggc cat ccc mac ttt ccc acd acc ctt ccc atc aaa cag      731
Phe Ser Gly His Pro Xaa Phe Pro Thr Thr Leu Pro Ile Lys Gln
                155                160                165
tgatgaacaa aatgatactc hsaagcmmct ttctgaagam caraacactg gaatattaca      791
agatgagatt ctgattcatg aagaaaagca gatagaagtg gctgaaaatg aattctgagc      851

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tttctcttag ttataaaaa gaaaaagacc tcttgcacga aaatagtagc ttgcaggaag 911
aaattgtcat gctaaactg gaactagack taatgaaaca tcagagccag ctaaraaaa 971
aaaaatattt ggaggaaatt gaaagtgtgg aaaaaaaaaa aa 1013
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<213> Homo sapiens

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<222> 46..693

<221> sig_peptide
<222> 46..90
<223> Von Heijne matrix
score 7.59999990463257
seq CVLVLAAAAGAVA/VF

<221> polyA_signal
<222> 937..942
<221> polyA_site
<222> 962..973

<400> 356
aaagcggctgg tccccggaag ttggacgcat gcgcccgtttc tctgc atg gtg tgc gtt 57
Met Val Cys Val
-15
ctc gtt cta gct gcg gcc gca gga gct gtg gcg gtt ttc cta atc ctg 105
Leu Val Leu Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
-10 -5 1 5
cga ata tgg gta gtg ctt cgt tcc atg gac gtt acg ccc cgg gag tct 153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
10 15 20
ctc agt atc ttg gta gtg gct ggg tcc ggt ggg cat acc act gag atc 201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
25 30 35
ctg agg ctg ctt ggg agc ttg tcc aat gcc tac tca cct aga cat tat 249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
40 45 50
gtc att gct gac act gat gaa atg agt gcc aat aaa ata aat tct ttt 297
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Asn Lys Ile Asn Ser Phe
55 60 65
gaa cta rat cga gsk gat aga rac cct agt aac atg twt acc aaa tac 345
Glu Leu Xaa Arg Xaa Asp Arg Xaa Pro Ser Asn Met Xaa Thr Lys Tyr
70 75 80 85
tac att cac cga att cca ara agc cgg gag gtt cag cag tcc tgg ccc 393
Tyr Ile His Arg Ile Pro Xaa Ser Arg Glu Val Gln Gln Ser Trp Pro
90 95 100
tcc acc gtt tyc acc acc ttg cac tcc atg tgg ctc tcc ttk ccc cta 441
Ser Thr Val Xaa Thr Thr Leu His Ser Met Trp Leu Ser Xaa Pro Leu
105 110 115
att cac agg gtg aag cca rat ttg gtg ttg tgt aac gga cca gga aca 489
Ile His Arg Val Lys Pro Xaa Leu Val Leu Cys Asn Gly Pro Gly Thr

120	125	130	
tgt gty cct atc tgt gta tct gcc ctt ctc ctt ggg ata cta gga ata	537		
Cys Val Pro Ile Cys Val Ser Ala Leu Leu Leu Gly Ile Leu Gly Ile			
135	140	145	
aag aaa gtg atc att gtc tac gtt gaa agc atc tgc cgt gta aaa acs	585		
Lys Lys Val Ile Ile Val Tyr Val Glu Ser Ile Cys Arg Val Lys Thr			
150	155	160	165
tta tcc atg tcc gga aag att ctg ttt cat ctc tca aat tac ttc att	633		
Leu Ser Met Ser Gly Lys Ile Leu Phe His Leu Ser Asn Tyr Phe Ile			
170	175	180	
gtt cag tgg ccg gct ctg aaa gaa aag tat ccc aaa tcg gtg tac ctt	681		
Val Gln Trp Pro Ala Leu Lys Glu Lys Tyr Pro Lys Ser Val Tyr Leu			
185	190	195	
ggg cga att gtt tgacaaatgg caactgactt ctttagaatt ttgcasttaa	733		
Gly Arg Ile Val			
200			
cagtartatg tactcaaatt ggggggaaaa aaaccctaca tgtttcttgt aaaggcgtct	793		
gacagtcctg araattattg atggtaagga ataaaaaatg twcagatrac tcagtgaara	853		
aactgaggct tctcttatga aacaaacatt gataaacgta actacyaaat gtttatgcct	913		
ctgtaaacca aatttctttt ctarataaaa atatgtatta ctacctgcaa aaaaaaaaaa	973		

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 <222> 126..527
 <221> sig_peptide
 <222> 126..182
 <223> Von Heijne matrix
 score 3.90000009536743
 seq ILFHGVFYAGGFA/IV

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<221> polyA_site
 <222> 856..867

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gcctttgatg attttcaaga gagttgtgct atgatgtggc aaagtatgca ggaagcaggc	120
ggtca atg cct ctg gga gca agg atc ctt ttc cac ggt gtg ttc tat gcc	170
Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala	
-15 -10 -5	
ggg ggc ttt gcc att gtg tat tac ctc att caa aag ttt cat tcc agg	218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg	
1 5 10	
act tta tat tac aag ttg gca gtg gar cag ctg car arc cat ccc gag	266
Thr Leu Tyr Tyr Lys Leu Ala Val Glu Gln Leu Gln Xaa His Pro Glu	
15 20 25	
gca cag gaa gct ctg ggc cct cct ctc aac atc cat tat ctc aag ctc	314

Ala	Gln	Glu	Ala	Leu	Gly	Pro	Leu	Asn	Ile	His	Tyr	Leu	Lys	Leu		
30						35				40						
atc	gac	agg	gaa	aac	ttc	gtg	gac	att	gtt	rat	gcc	aag	ttg	aaa	att	362
Ile	Asp	Arg	Glu	Asn	Phe	Val	Asp	Ile	Val	Xaa	Ala	Lys	Leu	Lys	Ile	
45					50					55					60	
cct	gtc	tct	gga	tcc	aaa	tca	gag	ggc	ctt	ctc	tac	gtc	cac	tca	tcc	410
Pro	Val	Ser	Gly	Ser	Lys	Ser	Glu	Gly	Leu	Leu	Tyr	Val	His	Ser	Ser	
				65					70					75		
aga	ggt	ggc	ccc	ttt	cag	agg	tgg	cac	ctt	gac	gag	gtc	ttt	tta	gag	458
Arg	Gly	Gly	Pro	Phe	Gln	Arg	Trp	His	Leu	Asp	Glu	Val	Phe	Leu	Glu	
			80					85					90			
ctc	aag	gat	ggt	cag	cag	att	cct	gtg	ttc	aag	ctc	agt	ggg	gaa	aac	506
Leu	Lys	Asp	Gly	Gln	Gln	Ile	Pro	Val	Phe	Lys	Leu	Ser	Gly	Glu	Asn	
			95				100						105			
ggg	gat	gaa	gtg	aaa	aag	gag	tagagacgac	ccagaagacc	cagcttgctt							557
Gly	Asp	Glu	Val	Lys	Lys	Glu										
			110			115										
ctagtccatc	cttccctcat	ctctaccata	tgccactgg	gggtggtggcc	catctcagtg											617
acagacactc	ctgcaaccca	gktttccagc	caccagtggg	atgatgggtat	gtgccagcac											677
atggtaattt	tggtgtaatt	ctaacttggg	cacaacgaat	gctatttgtc	atttttaaac											737
tgaatccgaa	agaaactcct	attataaatt	taagataatg	taatgtattt	gaaagtgcct											797
tgtataaaaa	agcacatgat	aaaaggaatc	agaattaata	aaatgtttgt	tgatctttaa											857
aaaaaaaaaa	h															868
<p><210> 358</p> <p><211> 519</p> <p><212> DNA</p> <p><213> Homo sapiens</p> <p><220></p> <p><221> CDS</p> <p><222> 66..320</p> <p><221> sig_peptide</p> <p><222> 66..113</p> <p><223> Von Heijne matrix</p> <p>score 3.5</p> <p>seq TALAAXTWLG VWG/VR</p> <p><221> polyA_signal</p> <p><222> 490..495</p> <p><221> polyA_site</p> <p><222> 508..519</p> <p><400> 358</p> <p>aattagcgcg taacgcasag actgcttgct gcggcagaga cgccagakgt gcagctccag 60</p> <p>cagca atg gca gtg acg gcg ttg gcg gcg mrg acg tgg ctt ggc gtg tgg 110</p> <p>Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp</p> <p>-15 -10 -5</p> <p>ggc gtg agg acc atg caa gcc cga ggc ttc ggc tcg gat cag tcc gag 158</p> <p>Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu</p> <p>1 5 10 15</p> <p>aat gtc gac cgg ggc gcg ggc tcc atc cgg gaa gcc ggt ggg gcc ttc 206</p> <p>Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe</p>																

	20		25		30	
gga aag aga gag cag gct gaa gag gaa cga tat ttc cga gca cag agt						254
Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser						
	35		40		45	
aca gaa caa ctg gca rct ttg aaa aaa crc cat gaa gaa gar atc gtt						302
Thr Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val						
	50		55		60	
cat cat aga gaa gga gat tgagcgtctg cagaaagaaa ttgagcgcca						350
His His Arg Glu Gly Asp						
	65					
taagcagaag atcaaaatgc tagaacatga tgattaagtg cacaccgtgt gccatagaat						410
ggcacatgtc attgccact tctgtgtaaa catggttctg gtttaactaa tatttgtctg						470
tgtgctacta acagattata ataaattgtc atcagtgaaa aaaaaaaaaa						519

<210> 359
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 <222> 73..948

<221> sig_peptide
 <222> 73..159
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 seq IVLHLVLQGMVYT/EY

<221> polyA_site
 <222> 1016..1028

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Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn	
	-25 -20
cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act	159
His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr	
	-15 -10 -5
gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc	207
Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser	
1 5 10 15	
ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt	255
Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe	
	20 25 30
ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca aaa gca	303
Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala	
	35 40 45
aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa ktg atg ttt	351
Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe	
	50 55 60
cca aaa aac gtg agg tgc tct act tgt gat tta agg aaa cca gct cga	399
Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg	
65 70 75 80	

tcc aas cac tgc akt gtg tgt aac tgg tgt gtg cac cgt ttc rac cat	447
Ser Xaa His Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His	
85 90 95	
cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc agg tmc	495
His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa	
100 105 110	
ttc ctc atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc gtc gcc	543
Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala	
115 120 125	
att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca gat tta	591
Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu	
130 135 140	
tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt atg gac	639
Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp	
145 150 155 160	
acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg att gtc	687
Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val	
165 170 175	
ttc atg ctg ggc ttt gtc gtg gtt ctg arc ttc ctc ctg ggt ggc tac	735
Phe Met Leu Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr	
180 185 190	
ctg ttg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac gag	783
Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu	
195 200 205	
tgg tac aga rgt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg gcc	831
Trp Tyr Arg Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala	
210 215 220	
tgg cct ccg tca gca gar ccc caa gtc cac cgg aac att cac tcc cat	879
Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His	
225 230 235 240	
ggg ctt cgg arc aac ctt caa gar atc ttt cta cct gcc ttt cca tgt	927
Gly Leu Arg Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys	
245 250 255	
cat gag agg aag aaa caa gaa tgacmagtgt atgactgcct ttgagctgta	978
His Glu Arg Lys Lys Gln Glu	
260	
gttccccgttt atttacacat gtggatcctc gttttccaaa aaaaaaaaaa	1028

<210> 360

<211> 452

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 69..434

<221> sig_peptide

<222> 69..236

<223> Von Heijne matrix
score 4.90000009536743
seq FACVPGASPTTLA/FP

<221> polyA_signal

<222> 419..424

<221> polyA_site

<222> 441..452

<400> 360

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gcgccgag atg acg ggc ttt ctg ctg ccg ccc gca agc aga ggg act cgg      110
    Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg
        -55                -50                -45
aga tca tgc agc aga agc aga aaa agg caa acg aga aga agg agg aac      158
Arg Ser Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn
        -40                -35                -30
cca agt agc ttt gtg gct tcg tgt cca acc ctc ttg ccc ttc gcc tgt      206
Pro Ser Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys
        -25                -20                -15
gtg cct gga gcc agt ccc acc acg ctc gcg ttt cct cct gta ktg ctc      254
Val Pro Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu
        -10                -5                1                5
aca ggt ccc avc acc gat ggc att ccc ttt gcc ctr nak tct gca gcg      302
Thr Gly Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala
        10                15                20
ggg ccc ttt tgt gct tcc ttc ccc tca ggt avc ctc tct ccc cct ggg      350
Gly Pro Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly
        25                30                35
cca ctc ccg ggg gtg agg ggg tta ccc ctt ccc agt gtt ttt tat tcc      398
Pro Leu Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser
        40                45                50
tgt ggg gct cac ccc aaa gta tta aaa gta gct ttg taattcaaaa      444
Cys Gly Ala His Pro Lys Val Leu Lys Val Ala Leu
        55                60                65
:: aaaaaaaaaa      452

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<210> 361

<211> 875

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 628..804

<221> sig_peptide

<222> 628..711

<223> Von Heijne matrix

score 4.19999980926514

seq LMPVIPALQEAXA/GG

<221> polyA_site

<222> 864..875

<400> 361

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cttagttcaa tggctgaaac acagtcgaaa agaatactgt gaattatgca agcacagatt      180
tgcttttaca ccaatttatt ctccagatat gccttcacgg cttccaattc aagacatatt      240

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tgctggactg gttacaagta ttggcactgc aatacgatat tggtttcatt atacacttgt 300
ggcctttgca tgggttgggag ttgttcctct tacagcatgt gaggattcat gcctctgatt 360
ggagttatatt aaacattgca taactactta atattataaaa gcaatattgc atcatattat 420
tatttgactg atgttttagtt atttgatgtc agagtgtcat gtattaggaa agccttactt 480
araaratgtt catcggaact aaraatgakt ttaacagggtc agtttttttga gtgaatgtgg 540
gaaaraacac agcatacaga atggctaacc atgaaagttc atgaaagcgt kgaaaaaatc 600
aatcaaatc ataattagat atgaagt atg cta rag ctt tca agg gct aca aaa 654

Met Leu Xaa Leu Ser Arg Ala Thr Lys

-25 -20

rac ggc cgg gcg cgg tgg ctt atg cct gta atc cca gca ctt cag gag 702
Xaa Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Ala Leu Gln Glu

-15 -10 -5

gcc gan gca ggc gga tca cga ggt cag gag ttt gaa act agc ctg gcc 750
Ala Xaa Ala Gly Gly Ser Arg Gly Gln Glu Phe Glu Thr Ser Leu Ala

1 5 10

aac atg gag act gag gca gga gaa ttg ctt aaa ccc agg agg cgg agg 798
Asn Met Glu Thr Glu Ala Gly Glu Leu Leu Lys Pro Arg Arg Arg Arg

15 20 25

ttg car tgaactgaga tcgcaccact gcactccagc ttgggcaaca gagcaagact 854
Leu Gln

30

ttgtctcgca aaaaaaaaaa a 875

<210> 362

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..366

<221> sig_peptide

<222> 70..108

<223> Von Heijne matrix

score 3.5

seq MHLLSNWANPASS/RR

<221> polyA_signal

<222> 496..501

<221> polyA_site

<222> 521..531

<400> 362

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cctcgagcgc atg cac ctc ctt tcc aac tgg gca aac ccc gct tcc agc aga 111

Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg

-10 -5 1

cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc 159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu

5 10 15

gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc 207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys

20 25 30

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tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac      255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
   35                40                45
agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca      303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
   50                55                60                65
cca atg aga aga tct tca tgc cat tta gaa tgt crg gtt ata ttc ctt      351
Pro Met Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu
           70                75                80
ttg gga cgc caa ttg taaktgttac cttcaaagga tttccttttc taaaaaatta      406
Leu Gly Arg Gln Leu
           85
ttttaratgt ctaactttat gttattgctc acgggtatatt gactgaattg ttgatttagg      466
ataagtcaat tcttgaggagg aaattaccaa ataaaatgat atgtattttct taccacaaaa      526
aaaaa                                           531

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<210> 363

<211> 1244

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..366

<221> sig_peptide

<222> 70..108

<223> Von Heijne matrix

score 3.5

seq MHLLSNWANPASS/RR

<221> polyA_site

<222> 1233..1244

<400> 363

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      Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg
           -10                -5                1
cgt cct tct atg gcc gct tca ggc act tct tgg ata tca tcg acc ctc      159
Arg Pro Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu
           5                10                15
gca cac tct ttg tca ctg aga gac gtc tca gag agg ctg tgc agc tgc      207
Ala His Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys
           20                25                30
tgg agg act ata agc atg gga ccc tgc gcc cgg ggg tca cca atg aac      255
Trp Arg Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn
           35                40                45
agc tct gga gtg cac aga aaa tca agc agg cta ttc tac atc cgg aca      303
Ser Ser Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr
           50                55                60                65
cca atg aga aga tct tca tgc cat tta raa tgt cag gtt ata ttc ctt      351
Pro Met Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu
           70                75                80
ttg gga cgc caa ttg tagtcgggtct tctcttgccc aaccagacac tggcatccac      406

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Leu Gly Arg Gln Leu

85

tgtcttctgg	cagtggctga	accagagcca	caatgcctgt	gtcaactatg	caaaccgcaa	466
tgcraccaag	ccttcacctg	catccaagtt	catccaggga	tacctgggag	ctgtcatcag	526
cgccgtctcc	attgtctgtg	gccttatktc	ctggttcaga	aagccaacaa	gttcacccca	586
gccacccgcc	ttctcatcca	gaggtttgtg	ccgttccttg	ctgtagccag	tgccaatatc	646
tgcaatgtgg	tcctgatgcg	gtacggggag	ctggaggaag	ggattgatgt	cctggacagc	706
gatggcaacc	tcgtgggctc	ctccaagatc	gcagcccgac	acgccctgct	ggagacggcg	766
ctgacgcgag	tggtcctgcc	catgcccac	ctggtgctac	ccccgatcgt	catgtccatg	826
ctggagaaga	cggctctcct	gcaggcacgc	ccccggctgc	tcctccctgt	gcaaagcctc	886
gtgtgcctgg	cagccttcgg	cctggccctg	ccgctggcca	tcagcctctt	cccgcaaagt	946
tcagagattg	aaacatccca	attagagccg	gagatagccc	aggccacgag	cagccggaca	1006
gtggtgtaca	acaaggggtt	gtgagtgtgg	tcagcggcct	ggggacggag	cactgtgcag	1066
ccggggagct	gaggggcarg	gccgtagact	cacggctgca	cctgcagggg	gcagcacgcc	1126
aaccccgagca	gtcctggggc	ccctggggaga	gtgctcaacc	tacagtggag	ggagactgac	1186
ccattcacat	tttaacatag	gcaagaggag	ttctaacaca	tttcgtacaa	aaaaaaaa	1244

<210> 364

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 111..434

<221> sig_peptide

<222> 111..185

<223> Von Heijne matrix

score 3.90000009536743

seq WIAAVTIAAGTAA/IG

<221> polyA_site

<222> 618..631

<400> 364

aatcgcgagg	tcgggtgcttt	agtacgccgc	tggcaccttt	actctcgccg	gccgcgcgaa	60
cccgtttgag	ctcggtatcc	tagtgcacac	gccttgcaag	cgacggcgcc	atg agt	116
					Met Ser	
					-25	
ctg act tcc	agt tcc agc	gta cga gtt	gaa tgg atc	gca gca gtt	acc	164
Leu Thr Ser	Ser Ser Ser	Val Arg Val	Glu Trp Ile	Ala Ala Val	Thr	
	-20		-15		-10	
att gct gct	ggg aca gct	gca att ggt	tat cta gct	tac aaa aga	ttt	212
Ile Ala Ala	Gly Thr Ala	Ala Ile Gly	Tyr Leu Ala	Tyr Lys Arg	Phe	
	-5		1		5	
tat gtt aaa	gat cat cga	aat aaa gct	atg ata aac	ctt cac atc	cag	260
Tyr Val Lys	Asp His Arg	Asn Lys Ala	Met Ile Asn	Leu His Ile	Gln	
10	15		20		25	
aaa gac aac	ccc aag ata	gta cat gct	ttt gac atg	gag gat ttg	gga	308
Lys Asp Asn	Pro Lys Ile	Val His Ala	Phe Asp Met	Glu Asp Leu	Gly	
	30		35		40	
gat aaa gct	gtg tac tgc	cgt tgt tgg	agg tcc aaa	aag ttc cca	ttc	356
Asp Lys Ala	Val Tyr Cys	Arg Cys Trp	Arg Ser Lys	Lys Lys Phe	Pro Phe	
	45		50		55	

tgt gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg	404
Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val	
60 65 70	
ggc cct ctg atc atc aag aaa aaa gaa act taaatggaca cttttgatgc	454
Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr	
75 80	
tgcaaatcag cttgtcgtga agttaccta ttgtttaatt araatgacta ccacctctgt	514
ctgattcacc ttcgctggat tctaaatgtg gtatattgcm aactgcagct ttcacattta	574
tggcatttgt cttgttgaaa catcgtgggtg cacatttggt taaacaaaaa aaaaaaa	631

<210> 365
 <211> 781
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 19..567

<221> sig_peptide
 <222> 19..63
 <223> Von Heijne matrix
 score 8.39999961853027
 seq AMWLLCVALAVLA/WG

<221> polyA_signal
 <222> 749..754
 <221> polyA_site
 <222> 771..781

<400> 365	
aagtgtctgct taccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg	51
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu	
-15 -10 -5	
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga	99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg	
1 5 10	
atg aag agt cgg gag cag gga aga cgg ctg gga gcc gaa agc cgg acc	147
Met Lys Ser Arg Glu Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr	
15 20 25	
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc	195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro	
30 35 40	
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc	243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys	
45 50 55 60	
ttc tct gca gga aat tac tac aat caa gga gag act cgt aag aaa gaa	291
Phe Ser Ala Gly Asn Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu	
65 70 75	
ctt ttg car agc tgt gat gtt ttg ggg att cca ctc tcc agt gta atg	339
Leu Leu Gln Ser Cys Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met	
80 85 90	
att att gac aac agg gat ttc cca rat gac cca ggc atg cag tgg gac	387
Ile Ile Asp Asn Arg Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp	

95	100	105	
aca rag cac gtg gcc ara gtc ctc ctt cag cac ata gaa gtg aat ggc			435
Thr Xaa His Val Ala Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly			
110	115	120	
atc aat ctg gtg gtg act ttc gat gca ggg gga rta agt ggc cac agc			483
Ile Asn Leu Val Val Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser			
125	130	135	140
aat cac att gct ctg tat gca gct gtg agg aag ctt gag ggc caa att			531
Asn His Ile Ala Leu Tyr Ala Ala Val Arg Lys Leu Glu Gly Gln Ile			
145	150	155	
tgc aag ccc tgt ggc act gga caa gac ttt aag gaa tgagtgtgt			577
Cys Lys Pro Cys Gly Thr Gly Gln Asp Phe Lys Glu			
160	165		
caatcagtgt gcctccacct tcaccatctt cttccctta ctctcacttc cgtcatgtgt			637
tttatacaac tctcaaactt ttcttgagga aggaggatat acatacataa tatgaaatgt			697
gtttgttctt cacagtcacc cgattttact gatattttatt tgcattttac caataaaaag			757
aaaatgcaag ctcaaaaaaa aaaa			781

<210> 366
 <211> 931
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 19..312
 <221> sig_peptide
 <222> 19..63
 <223> Von Heijne matrix
 score 8.39999961853027
 seq AMWLLCVALAVLA/WG
 <221> polyA_signal
 <222> 896..901
 <221> polyA_site
 <222> 921..931

<400> 366	
aagtgtgtgt tacccatc atg gaa gca atg tgg ctc ctg tgt gtg gcg ttg	51
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu	
-15 -10 -5	
gcg gtc ttg gca tgg ggc ttc ctc tgg gtt tgg gac tcc tca gaa cga	99
Ala Val Leu Ala Trp Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg	
1 5 10	
atg aag agt cgg gag cag gga rga cgg ctg gga gcc gaa agc cgg acc	147
Met Lys Ser Arg Glu Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr	
15 20 25	
ctg ctg gtc ata gcg cac cct gac gat gaa gcc atg ttt ttt gct ccc	195
Leu Leu Val Ile Ala His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro	
30 35 40	
aca gtg cta ggc ttg gcc cgc cta agg cac tgg gtg tac ctg ctt tgc	243
Thr Val Leu Gly Leu Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys	
45 50 55 60	

ttc tct gca gtt ttc cgt agg gag cta agt gaa tac acc gaa rgt ctt	291
Phe Ser Ala Val Phe Arg Arg Glu Leu Ser Glu Tyr Thr Glu Xaa Leu	
65 70 75	
acc tct gaa ccc ctc ama gcc tagggacagg arcggccggc ttacctgggtg	342
Thr Ser Glu Pro Leu Xaa Ala	
80	
ggttggggga cgtcggcagc tcrctacta cgccagcagg attganganc acagaaacag	402
ttgchsttgg ttgtattcag tacctkcatt tccgttggga actccaccwg tacttgttat	462
kctgtggaac ttttttttat ttgtagaagg agcaagaata ttgaccttac tatatagcac	522
acgaaacaat ctatgctgta tcgtgcctgc tcaatcctta aagttaactt ctaatgatag	582
taaaaracct tcctgctgcc tttaaaatgc agcttgtgct aktaacatgc atgtgtcaaaa	642
ttgaaraatt agacatagat gactaratar aaagtaattt tgtaggtaat ttaragttc	702
aactccaccc agctttcakt gaaggaacct ttcaaataat aratttttgc ttaccatara	762
raaaaratca aatgacaaaag caaatattga ccattaagct ggaatatggg gataattgaa	822
cagttgtata aatgaaktaa ttgaattgta cacatacaat ggggtgaattt tatggcatgt	882
caaagtatac ctcaataaag ctattttttt aaattgcmaa aaaaaaaaaa	931

<210> 367

<211> 849

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 64..612

<221> sig_peptide

<222> 64..234

<223> Von Heijne matrix

score 3.79999995231628

seq QLWLVMFCGAGS/VT

<221> polyA_site

<222> 839..849

<400> 367

acatacgggc aagtttataa gggtcgtcat gtcaaaacgg gccagcttgc agccatcaag	60
ggt atg gat gtc aca ggg gat gaa gag gaa gaa atc aaa caa gaa att	108
Met Asp Val Thr Gly Asp Glu Glu Glu Glu Ile Lys Gln Glu Ile	
-55 -50 -45	
aac atg ttg aag aaa tat tct cat cac cgg aat att gct aca tac tat	156
Asn Met Leu Lys Lys Tyr Ser His His Arg Asn Ile Ala Thr Tyr Tyr	
-40 -35 -30	
ggt gct ttt atc aaa aag aac cca cca ggc atg gat gac caa ctt tgg	204
Gly Ala Phe Ile Lys Lys Asn Pro Pro Gly Met Asp Asp Gln Leu Trp	
-25 -20 -15	
ttg gtg atg gag ttt tgt ggt gct ggc tct gtc acc gac ctg atc aag	252
Leu Val Met Glu Phe Cys Gly Ala Gly Ser Val Thr Asp Leu Ile Lys	
-10 -5 1 5	
aac aca aaa ggt aac acg ttg aaa gag gag tgg att gca tac atc tgc	300
Asn Thr Lys Gly Asn Thr Leu Lys Glu Glu Trp Ile Ala Tyr Ile Cys	
10 15 20	
msg gaa atc tta cgg ggg ctg art cac ctg cac cag cat aaa gtg att	348
Xaa Glu Ile Leu Arg Gly Leu Xaa His Leu His Gln His Lys Val Ile	
25 30 35	

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cat cga rat att aaa ggg caa aat gtc ttg ctg act gaa aat gca gaa      396
His Arg Xaa Ile Lys Gly Gln Asn Val Leu Leu Thr Glu Asn Ala Glu
   40                               45                               50
gtt aaa cta gtg gac ttt gga rtc akt gct cag ctt gat cga aca gtg      444
Val Lys Leu Val Asp Phe Gly Xaa Xaa Ala Gln Leu Asp Arg Thr Val
   55                               60                               65                               70
ggc agg arg aat act ttc att gga act ccc tac tgg atg gca cca raa      492
Gly Arg Xaa Asn Thr Phe Ile Gly Thr Pro Tyr Trp Met Ala Pro Xaa
                               75                               80                               85
gtt att gcc tgt gat gaa aac cca sat gcc aca tat gat ttc aar art      540
Val Ile Ala Cys Asp Glu Asn Pro Xaa Ala Thr Tyr Asp Phe Lys Xaa
                               90                               95                               100
gac ttg tgg tct ttg ggt atc acc gcc att gaa atg gca gaa ggg ctc      588
Asp Leu Trp Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Leu
                               105                               110                               115
ccc ctc tct gtg aca tgc acc cca tgagagctct cttctcatc ccccggaatc      642
Pro Leu Ser Val Thr Cys Thr Pro
                               120                               125
cagcgcctcg gctgaagtct aagaagtggc caaaaaaatt ccagtcattt attgagagct      702
gcttggtataa aaatcacagc cagcgaccag caacagaaca attgatgaag catccattta      762
tacgagacca acctaattgag cgacaggtcc gcattcaact caaggacatc attgatagaa      822
caaaagaagaa gcgaggaaaa aaaaaaaa      849

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<210> 368

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..458

<221> sig_peptide

<222> 39..80

<223> Von Heijne matrix

score 4.40000009536743

seq FLTALLWRGRIPG/RQ

<221> polyA_signal

<222> 613..618

<221> polyA_site

<222> 633..644

<400> 368

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agcggagacg cagagtcttg agcagcgcgcn caggcacc atg ttc ctg act gcg ctc      56
                               Met Phe Leu Thr Ala Leu
                               -10
ctc tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg      104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg
                               -5                               1                               5
cgg ccg cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc      152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg
                               10                               15                               20
ctg gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg      200

```

```

Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met
25          30          35          40
acc cgg gag cag gag cgc ggc cac gcc gcg ttg cgc agg agg gag gcc      248
Thr Arg Glu Gln Glu Arg Gly His Ala Ala Leu Arg Arg Arg Glu Ala
          45          50          55
ttc gag gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga      296
Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg
          60          65          70
ttc att gcg gac cag ctc gac cat ctc aat vgt cac caa gaa atg gtc      344
Phe Ile Ala Asp Gln Leu Asp His Leu Asn Xaa His Gln Glu Met Val
          75          80          85
cta atc ctg agt cgt cac cct tgg att tta tgg atc acg gag ctg acc      392
Leu Ile Leu Ser Arg His Pro Trp Ile Leu Trp Ile Thr Glu Leu Thr
          90          95          100
atc ttt acc tgg tct gga ctg aaa aac tgt agc ttg tgt gaa aat gag      440
Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys Ser Leu Cys Glu Asn Glu
105          110          115          120
ctt tgg acc agt ctt tat taaaacaaac aaacatgagt agtctgcata      488
Leu Trp Thr Ser Leu Tyr
          125
tcgaatatct agagctctaa accccccaat acttaaaagt ctaattgctg tcctgtgggt      548
tcattagtct gataggaaga tagggatttc ctcagtcaca gatgatattt tgaaggaaag      608
ctgcaataaa gccacaatga tttgaaaaaa aaaaaa      644

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<210> 369

<211> 918

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 9..185

<221> sig_peptide

<222> 9..50

<223> Von Heijne matrix
score 3.70000004768372
seq AALVTVLFTGVRR/LH

<221> polyA_site

<222> 906..918

<400> 369

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agctcagc atg gct gct tta gtg act gtt ctc ttc aca ggt gtc cgg agg      50
      Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg
          -10          -5
ctg cac tgc agc gcr scg ctt ggg cgg gcg gcc agt ggc grc tac agc      98
Leu His Cys Ser Ala Xaa Leu Gly Arg Ala Ala Ser Gly Xaa Tyr Ser
1          5          10          15
agg aac tgg ctg cca acc cct ccg gct acg ggc ccc tta ccg agc tcc      146
Arg Asn Trp Leu Pro Thr Pro Pro Ala Thr Gly Pro Leu Pro Ser Ser
          20          25          30
cag act ggt cat atg cgg atg gcc gcc ctg ctc ccc caa tgaaaggcca      195
Gln Thr Gly His Met Arg Met Ala Ala Leu Leu Pro Gln
          35          40          45

```



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gcttcgaaaa aaagctgaaa gggagacktt tgcaaracra kttgtactgc tgtcacagga 255
aatggacgct ggattacaas catggcasct caggcagcar aakttgcagg aaraacaaaag 315
gaagcaggaa aatgctctta aacccaaagg ggcttcactg aaaascccac ttccaaktca 375
ataaaaagca actcctgcct cccttcctca ccctgtctct ggatttcttt tctatcacct 435
aratgcttca tccagccara aaatagcctt cackktcccc atctgtcttc aragcaaaar 495
agctgggacm ccaaraacaa gctgttarat cactgcctgg gaggcttggc ttartactct 555
catctctggt tccattccag ttcagetaag tcttgcttta aaatttttac ctccctagctg 615
ggtgcggtgg ctcacgcctg taatcccagc actttggggag gctgaggcgg gcagatcaca 675
agatcaggag ttcgagacca gcctggccaa cccagcctgg tcaacatggt gaaaccctgt 735
ccctactaaa gatacaaaac attagccggg cgtggtgggg tgcgcttgta atcccagcta 795
ctcaggaggc tgaggcagga gaatcgctta aactcggggag gtagagggtg cagttagcca 855
aggtcacacc attgcactcc aacctgggag acagggcgag actctgtctc aaaaaaaaaa 915
aaa 918

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<210> 370

<211> 472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 14..316

<221> sig_peptide

<222> 14..121

<223> Von Heijne matrix

score 5.19999980926514

seq PLRLNLLILIEG/SV

<221> polyA_signal

<222> 442..447

<221> polyA_site

<222> 458..471

<400> 370

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attatataga gcc atg ggg cct tac aac gtg gca gtg cct tca gat gta 49
          Met Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val
          -35          -30          -25
tct cat gcc cgc ttt tat ttc tta ttt cat cga cca tta agg ctg tta 97
Ser His Ala Arg Phe Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu
          -20          -15          -10
aat ctg ctc atc ctt att gag ggc agt gtc gtc ttc tat cag ctc tat 145
Asn Leu Leu Ile Leu Ile Glu Gly Ser Val Val Phe Tyr Gln Leu Tyr
          -5          1          5
tcc ttg ctg cgg tcg gag aag tgg aac cac aca ctt tcc atg gct ctc 193
Ser Leu Leu Arg Ser Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu
          10          15          20
atc ctc ttc tgc aac tac tat gtt tta ttt aaa ctt ctc cgg gac aga 241
Ile Leu Phe Cys Asn Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg
          25          30          35          40
wta kta tta ggc agg gca tac tcc tac cca ctc aac agt tat gaa ctc 289
Xaa Xaa Leu Gly Arg Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu
          45          50          55
aag gca aac twa gct gcc tct caw caa tgaggggagaa ctcagataaa 336

```

Lys Ala Asn Xaa Ala Ala Ser Xaa Gln

60 65

aatatatttca	tacgttctat	ttttttcttg	tgatttttat	aaatatattaa	gatattttat	396
atattgtata	ctattatggt	ttgaaagtcg	ggaagagtaa	gggatattaa	atgtatccgt	456
aaacaaaaaa	aaaaaam					472

<210> 371

<211> 1504

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..1092

<221> sig_peptide

<222> 70..234

<223> Von Heijne matrix

score 4.09999990463257

seq AVCAALLASHPTA/EV

<221> polyA_signal

<222> 1475..1480

<221> polyA_site

<222> 1493..1504

<400> 371

agaaatcgta	ggacttccga	aagcagcggc	ggcgtttgct	tcactgcttg	gaagtgtgag	60
tgcgcgaaag	atg cga aag	gtg gtt ttr	att acc ggg	gct agc agt	ggc att	111
	Met Arg Lys	Val Val Leu	Ile Thr Gly	Ala Ser Ser	Gly Ile	
	-55	-50	-45			
ggc ctg gcc	ctc tgc aag	cgg ctg ctg	gcg gaa gat	gat gag ctt	cat	159
Gly Leu Ala	Leu Cys Lys	Arg Leu Leu	Ala Glu Asp	Asp Glu Leu	His	
	-40	-35	-30			
ctg tgt ttg	gcg tgc agg	aat atg agc	aag gca gaa	gct gtc tgt	gct	207
Leu Cys Leu	Ala Cys Arg	Asn Met Ser	Lys Ala Glu	Ala Val Cys	Ala	
	-25	-20	-15	-10		
gct ctg ctg	gcc tct cac	ccc act gct	gag gtc acc	att gtc cag	gtg	255
Ala Leu Leu	Ala Ser His	Pro Thr Ala	Glu Val Thr	Ile Val Gln	Val	
	-5	1	5			
gat gtc agc	aac ctg cag	tca ttc ttc	cgg gcc tcc	aag gaa ctt	aag	303
Asp Val Ser	Asn Leu Gln	Ser Phe Phe	Arg Ala Ser	Lys Glu Leu	Lys	
	10	15	20			
caa agg ttt	cag aga tta	gac tgt ata	tat cta aat	gct ggg atc	atg	351
Gln Arg Phe	Gln Arg Leu	Asp Cys Ile	Tyr Leu Asn	Ala Gly Ile	Met	
	25	30	35			
cct aat cca	caa cta aat	atc aaa gca	ctt ttc ttt	ggc ctc ttt	tca	399
Pro Asn Pro	Gln Leu Asn	Ile Lys Ala	Leu Phe Phe	Gly Leu Phe	Ser	
	40	45	50	55		
aga aaa gtg	att cat atg	ttc tcc aca	gct gaa ggc	ctg ctg acc	cag	447
Arg Lys Val	Ile His Met	Phe Ser Thr	Ala Glu Gly	Leu Leu Thr	Gln	
	60	65	70			
ggg gat aag	atc act gct	gat gga ctt	cag gag gtg	ttt gag acc	aat	495
Gly Asp Lys	Ile Thr Ala	Asp Gly Leu	Gln Glu Val	Phe Glu Thr	Asn	

	75		80		85	
gtc ttt ggc cat ttt atc ctg att cgg gaa ctg gag cct ctc ctc tgt						543
Val Phe Gly His Phe Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys						
	90		95		100	
cac agt gac aat cca tct cag ctc atc tgg aca tca tct cgc agt gca						591
His Ser Asp Asn Pro Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala						
	105		110		115	
agg aaa tct aat ttc agc ctc gag gac ttc cag cac agc aaa ggc aag						639
Arg Lys Ser Asn Phe Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys						
	120		125		130	135
gaa ccc tac agc tct tcc aaa tat gcc act gac ctt ttg agt gtg gct						687
Glu Pro Tyr Ser Ser Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala						
	140		145		150	
ttg aac agg aac ttc aac cag cag ggt ctc tat tcc aat gtg gcc tgt						735
Leu Asn Arg Asn Phe Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys						
	155		160		165	
cca ggt aca gca ttg acc aat ttg aca tat gga att ctg cct ccg ttt						783
Pro Gly Thr Ala Leu Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe						
	170		175		180	
ata tgg acg ctg ttg atg ccg gca ata ttg cta ctt cgc ttt ttt gca						831
Ile Trp Thr Leu Leu Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala						
	185		190		195	
aat gca ttc act ttg aca cca tat aat gga aca gaa gct ctg gta tgg						879
Asn Ala Phe Thr Leu Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp						
	200		205		210	215
ctt ttc cac caa aag cct gaa tct ctc aat cct ctg atc aaa tat ctg						927
Leu Phe His Gln Lys Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu						
	220		225		230	
agt gcc acc act ggc ttt gga aga aat tac att atg acc cag aag atg						975
Ser Ala Thr Thr Gly Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met						
	235		240		245	
gac cta gat gaa gac act gct gaa aaa ttt tat caa aag tta ctg gaa						1023
Asp Leu Asp Glu Asp Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu						
	250		255		260	
ctg gaa aag cac att agg gtc act att caa aaa aca gat aat cag gcc						1071
Leu Glu Lys His Ile Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala						
	265		270		275	
agg ctc agt ggc tca tgc cta taattccagc actttgggag gccaaaggcag						1122
Arg Leu Ser Gly Ser Cys Leu						
	280		285			
aaggatcact tgagaccagg agttcaagac cagcctgaga aacatagtga gcccttgtct						1182
ctacaaaaag aaataaaaaat aatagctggg tgtgggtggca tgcgcatgta gtcccagcta						1242
ctcagaagga tgaggtggga ggatctcttg aggctgggag gcagaggttg cagtgagctg						1302
agattgtgcc actgcactcc agcctgggtg acagcgagac cctgtctcaa aatatgtata						1362
tatttaatat atatataaaa ccagagctga caatgacact ctggaacatt gcataccttc						1422
tgtacattct ggggtacatg gatttctact gagttggata atatgcattt gtaataaaact						1482
atgaactatg aaaaaaaaaa aa						1504

<210> 372

<211> 765

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 274..597

<221> sig_peptide

<222> 274..399

<223> Von Heijne matrix

score 5.19999980926514

seq LLFDLVCHEFCQS/DD

<221> polyA_signal

<222> 731..736

<221> polyA_site

<222> 754..765

<400> 372

accaggaaca	tccagctatt	tatgatagca	tttgcttcat	tatgtcaagt	tcaacaaatg	60
ttgacttgct	ggtgaagggtg	ggggagggtt	tggaacaagct	ctttgatttg	gatgagaaac	120
taatgttaag	aatgggtcag	aaatggggct	gctcagcctc	tggaaccaacc	ccaggaagag	180
tctgaagagc	agccagtgtt	tcggcttgtg	ccctgtatac	ttgaagctgc	caaacaagta	240
cgttctgaaa	atccagaatg	gcttgatggt	tac atg cac	att tta caa	ctg ctt	294

Met His Ile Leu Gln Leu Leu

-40

act	aca	gtg	gat	gat	gga	att	caa	gca	att	gta	cat	tgt	cct	gac	act	342
Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala	Ile	Val	His	Cys	Pro	Asp	Thr	
35					-30					-25					-20	
gga	aaa	gac	att	tgg	aat	tta	ctt	ttt	gac	ctg	gtc	tgc	cat	gaa	ttc	390
Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe	Asp	Leu	Val	Cys	His	Glu	Phe	
					-15					-10					-5	
tgc	cag	tct	gat	gat	cca	gcc	atc	att	ctt	caa	raa	car	aaa	acr	gtg	438
Cys	Gln	Ser	Asp	Asp	Pro	Ala	Ile	Ile	Leu	Gln	Xaa	Gln	Lys	Thr	Val	
					1					5					10	
cta	gcc	tct	ggt	ttt	tca	gtg	ttg	tct	gcc	atc	tat	gcc	tca	cag	act	486
Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser	Ala	Ile	Tyr	Ala	Ser	Gln	Thr	
	15					20				25						
gag	caa	gak	tat	cta	aar	ata	raa	aaa	gga	gac	ggg	ggc	tca	ggg	agt	534
Glu	Gln	Xaa	Tyr	Leu	Lys	Ile	Xaa	Lys	Gly	Asp	Gly	Gly	Ser	Gly	Ser	
30					35					40					45	
aaa	gga	agg	cca	ktt	gan	caa	aca	gaa	ktg	ttc	ctc	tgc	att	tca	aaa	582
Lys	Gly	Arg	Pro	Xaa	Xaa	Gln	Thr	Glu	Xaa	Phe	Leu	Cys	Ile	Ser	Lys	
					50					55					60	
cct	tct	tcc	ttt	cta	tagccctgtg	gtggaagatt	ttattaaaat	cctacgtgaa								637
Pro	Ser	Ser	Phe	Leu												
					65											
gttgataagg	cgcttgctga	tgacttggaa	aaaaacttcc	caagtttgaa	ggttcagact											697
taaaacctga	attggaatta	cttctgtaca	agaaataaac	tttatttttc	tcactgacaa											757
aaaaaaaa																765

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<211> 1041

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 230..469

<221> sig_peptide

<222> 230..307

<223> Von Heijne matrix

score 4.90000009536743

seq VLCTNQVLITARA/VP

<221> polyA_signal

<222> 1004..1009

<221> polyA_site

<222> 1027..1040

<400> 373

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aacttccaag ttgtagtggt gttgtttttca gcctgctgct gctgctgcta ttgcggctag      60
gggaaccgtc gtgggggaagg atggtgtgctg aaaaatgtga aaagaaactt ggtactgtta      120
tactccaga tacatggaaa gatggtgcta ggaataccac agaaagtggg ggaagaaagc      180
tgaatgaaaa taaagctttg acttcaaaaa aagccagaat tgatccata atg gaa gaa      238
                                   Met Glu Glu
                                   -25
ata agt tct cca ctt gta gaa ttt gta aaa gtt ttg tgc acc aac cag      286
Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
                                   -20               -15               -10
gtt ctc att act gcc agg gct gtg cct aca aaa aag gca tct gtg cga      334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
                                   -5               1               5
tgt gtg gaa aaa agg ttt tgg ata cca aaa act aca agc aaa cat ctg      382
Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
10               15               20               25
tct aga tgt att gat gga att tct ggc ttt cta aat gat ttt act ttc      430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
                                   30               35               40
tgc ctt gaa ttt tca agg cat aga tgt caa ctt aca gaa taacatgkt      479
Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
                                   45               50
taagataatt aagtktaaac cagaraattt gattgttact catttttgctc tcatgktcta      539
aaacagcaac agtgtaacta gtctttttgtt gtaaattggtt attttcctta taaaaatttt      599
aaaaactaag tggcaaattc catgaaaata tttctcagtt ctgtatgcac ttttatttaa      659
cattattcat ataattctcc cccaccact ttatttataa atactgcaaa aktgaraagg      719
agataataaa tacttttgctc tgaatttggc atccaaagtt aacattttctc ccctcactcc      779
cttgctgggtg tcatagttat tagaatcagc agcctcttaa ctaattgcgg tttcatagga      839
tatataaatg tttcaagcca ttattgctga atggttcttt agttattaac ctagacccaa      899
atcaaagacc agttggattt atgatatttt ttatttggtc ttgcagccaa agtgccagtt      959
tctttaatat gtgaccaaga acacaaggag catccatattg gccaaataaa tacactgaat      1019
tttagaaaaa caaaaaaaaa ar      1041

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<210> 374

<211> 1164

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 72..545

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 <222> 72..203
 <223> Von Heijne matrix
 score 5.5
 seq ILFFTGWWIMIDA/AV

<221> polyA_site
 <222> 1151..1162

<400> 374

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aagaagtaaa a atg gca ggc ttc cta gat aat ttt cgt tgg cca gaa tgt      110
          Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys
                    -40                    -35

gaa tgt att gac tgg agt gag aga aga aat gct gtg gca tct gtt gtc      158
Glu Cys Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val
          -30                    -25                    -20

gca ggt ata ttg ttt ttt aca ggc tgg tgg ata atg att gat gca gct      206
Ala Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
          -15                    -10                    -5                    1

gtg gtg tat cct aag cca gaa cag ttg aac cat gcc ttt cac aca tgt      254
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys
                    5                    10                    15

ggg gta ttt tcc aca ttg gct ttc ttc atg ata aat gct gta tcc aat      302
Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn
                    20                    25                    30

gct cag gtg aga ggt gat agc tat gaa agc ggc tgt tta gga aga aca      350
Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr
                    35                    40                    45

ggg gct cga gtt tgg ctt ttc att ggt ttc atg ttg atg ttt ggg tca      398
Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser
          50                    55                    60                    65

ctt att gct tcc atg tgg att ctt ttt ggt gca tat gtt acc caa aat      446
Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn
                    70                    75                    80

act gat gtt tat ccg gga cta gct gtg ttt ttt caa aat gca ctt ata      494
Thr Asp Val Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile
                    85                    90                    95

ttt ttt agc act ctg atc tac aaa ttt gga aga acc gaa gag cta tgg      542
Phe Phe Ser Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp
                    100                    105                    110

acc tgagatcact tcttaagtca cattttcctt ttgttatatt ctgtttgtag      595
Thr

ataggttttt tatctctcag tacacattgc caaatggagt agattgtaca ttaaatgttt      655
tgtttcttta catttttatg ttctgagttt tgaaatagtt ttatgaaatt tctttatatt      715
tcattgcata gactgttaat atgtatataa tacaagacta tatgaattgg ataatgagta      775
tcagtttttt attcctgaga tttagaactt gatctactcc ctgagccagg gttacatcat      835
cttgtcattt tagaagtaac cactcttgtc tctctggctg ggcacgggtg ctcatgcctg      895
taatcccagc actttgggag gccgaggcgg gccgattgct tgaggtcaag tgtttgagac      955
cagcctggcc aacatggcga aaccccatct actaaaaata caaaaattag ccaggcatgg      1015
tggtgggtgc ctgtaatccc aactacctag gaggtgagg caggagaatc gcttgaacct      1075
ggggggcaga gggtgyagtg agctgagttt gcgccactgc actctagcct gggggagaaa      1135
gtgaaactcc ctctcaaaaa aaaaaaamc      1164
    
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<210> 375

<211> 1250
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 36..425

<221> sig_peptide
<222> 36..119
<223> Von Heijne matrix
score 11.6000003814697
seq LLLLVQLLRFLRA/DG

<221> polyA_signal
<222> 1215..1220

<221> polyA_site
<222> 1240..1250

<400> 375

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                                Met Asn Trp Glu Leu Leu
                                -25
ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc ttg gtg cag ctg      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Leu Val Gln Leu
-20 -15 -10
ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta cta tgg gcc gag      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5 1 5 10
tgg cag gga cga cgc cca gaa tgg gag ctg act gat atg gtg gtg tgg      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
15 20 25
gtg act gga gcc tcg agt gga att ggt gag gag ctg gct tac cag ttg      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
30 35 40
tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga aga gtg cat gag      293
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg Arg Val His Glu
45 50 55
ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc aat tta aaa gaa      341
Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly Asn Leu Lys Glu
60 65 70
aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac act ggt tcc cat      389
Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp Thr Gly Ser His
75 80 85 90
gaa agc ggc tac caa agc tgt tct cca gga att tgg tagaatcgac      435
Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly Ile Trp
95 100
attctggtca acaatgtgga aatgtcccag cggtctctgt gcatggatac caacttggat      495
gtctacagaa agctaattgag agcttaacta cttagggacg gtgtccttga caaaatgtgk      555
kctgcctcac atgatcgaga ngaarcaagg aaagattgtt actgtgaata gcatcctggg      615
tatcatactt gtacctcttt ccattggata ctgtgctagc aagcatgctc tccgggggk      675
ktttaattggc cttcraacag aacttgccac ataccargt ataatagttt ctaacatttg      735
cccaggacct gtgcaatcaa atattgtgga aaattcccta gctggagaag tcacaaagac      795
tataggcaat aatggagacc agtcccacaa gatgacaacc agtcgtttgtg tgcggctgat      855
gttaatcagc atggccaatg atttgaaaga agtttgatc tcagaacaac ctttcttggt      915
agtaacatat ttgtggcaat acatgcccaac ctgggcctgg tggataacca acaagatggg      975

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gaagaaaagg attgagaact ttaagagtgg tgtggatgca gactcttctt attttaaaat 1035
ctttaagaca aaacatgact gaaaagagca cctgtacttt tcaagccact ggagggagaa 1095
atggaaaaca tgaaaacagc aatcttctta tgcttctgaa taatcaaaga ctaatttgtg 1155
attttacttt ttaatagata tgactttgct tccaacatgg aatgaaataa aaaataaata 1215
ataaaaagatt gccatgaatc ttgcaaaaaa aaaaa 1250
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<210> 376
<211> 947
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 155..751

<221> sig_peptide
<222> 155..340
<223> Von Heijne matrix
score 3.70000004768372
seq SILGIISVPLSIG/YC

<221> polyA_signal
<222> 912..917

<221> polyA_site
<222> 937..947

<400> 376
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ccttgacctg accgacactg gttcccatga agcggctacc aaagctgttc tccaggagtt 120
tggtagaatc gacattctgg tcaacaatgg tgga atg tcc cag cgt tct ctg tgc 175
Met Ser Gln Arg Ser Leu Cys
-60
atg gat acc agc ttg gat gtc tac aga rag cta ata gag ctt aac tac 223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55 -50 -45 -40
tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc gag 271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
-35 -30 -25
agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc ata 319
Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
-20 -15 -10
tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc cgg 367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg
-5 1 5
ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt ata 415
Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile
10 15 20 25
ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg gaa 463
Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu
30 35 40
aat tcc cta gct gga gaa gtc aca aaa act ata ggc aat aat gga aac 511
Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asn
45 50 55
cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta atc 559

Gln	Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	
	60						65					70				
agc	atg	gcc	aat	gat	ttg	aaa	gaa	gtt	tgg	atc	tca	gaa	caa	cct	ttc	607
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	Phe	
	75					80				85						
ttg	tta	gta	aca	tat	ttg	tgg	caa	tac	atg	cca	acc	tgg	gcc	tgg	tgg	655
Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	Trp	Trp	
90					95				100					105		
ata	acc	aac	aag	atg	ggg	aag	aaa	agg	att	gag	aac	ttt	aag	agt	ggg	703
Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	Lys	Ser	Gly	
			110					115				120				
gtg	gat	gcm	rac	tct	tct	tat	ttt	aaa	atc	ttt	aag	aca	aaa	cat	gac	751
Val	Asp	Ala	Xaa	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	Thr	Lys	His	Asp	
			125				130				135					
tgaaaaganc	acctgtactt	ttcaagccac	tgaggaggaga	aatggaaaac	atgaaaacag											811
caatcttctt	atgcttctga	ataatcaaag	actaatttgt	gattttactt	tttaatagat											871
atgactttgc	ttccaacatg	grrtgaaata	aaaaataaat	aataaaaagat	tgccatgrrt											931
cttgcaaaaa	aaaaaa															947

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 <222> 46..585
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 score 6.30000019073486
 seq AFSLSVMAALTFG/CF
 <221> polyA_signal
 <222> 584..589
 <221> polyA_site
 <222> 606..619

<400> 377																
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						Met	Asn	Thr	Val							
						-25										
ctg	tcg	cgg	gcg	aac	tca	ctg	ttc	gcc	ttc	tcg	ctg	agc	gtg	atg	gcs	105
Leu	Ser	Arg	Ala	Asn	Ser	Leu	Phe	Ala	Phe	Ser	Leu	Ser	Val	Met	Ala	
-20						-15					-10					
gcg	ctc	acc	ttc	ggc	tgc	ttc	atc	ayy	acc	gcc	ttc	aaa	gac	agg	agc	153
Ala	Leu	Thr	Phe	Gly	Cys	Phe	Ile	Xaa	Thr	Ala	Phe	Lys	Asp	Arg	Ser	
-5				1				5					10			
gtc	ccg	gtg	cgg	ctg	cac	gtc	tcg	cga	atc	atg	cta	aaa	aat	gta	gaa	201
Val	Pro	Val	Arg	Leu	His	Val	Ser	Arg	Ile	Met	Leu	Lys	Asn	Val	Glu	
			15				20				25					
gat	ttc	act	gga	cct	aga	gaa	aga	agt	gat	ctg	gga	ttt	atc	aca	ttt	249
Asp	Phe	Thr	Gly	Pro	Arg	Glu	Arg	Ser	Asp	Leu	Gly	Phe	Ile	Thr	Phe	

30	35	40	
gat ata act gct gat cta gag aat ata ttt gat tgg aat gtt aag cag			297
Asp Ile Thr Ala Asp Leu Glu Asn Ile Phe Asp Trp Asn Val Lys Gln			
45	50	55	
ttg ttt ctt tat tta tca gca gaa tat tca aca aaa aat aat gct ctg			345
Leu Phe Leu Tyr Leu Ser Ala Glu Tyr Ser Thr Lys Asn Asn Ala Leu			
60	65	70	75
aac caa ktt gtc cta tgg gac aag att gtt ttg aga ggt gat aat ccg			393
Asn Gln Xaa Val Leu Trp Asp Lys Ile Val Leu Arg Gly Asp Asn Pro			
80	85	90	
aag ctg ctg ctg aaa gat atg aaa aca aaa tat ttt ttc ttt gac gat			441
Lys Leu Leu Leu Lys Asp Met Lys Thr Lys Tyr Phe Phe Phe Asp Asp			
95	100	105	
gga aat ggt ctc wag gga aac agg aat gtc act ttg acc ctg tct tgg			489
Gly Asn Gly Leu Xaa Gly Asn Arg Asn Val Thr Leu Thr Leu Ser Trp			
110	115	120	
aac gtc gta cca aat gct gga att cta cct ctt gtg aca gga tca gga			537
Asn Val Val Pro Asn Ala Gly Ile Leu Pro Leu Val Thr Gly Ser Gly			
125	130	135	
cac gta tct gtc cca ttt cca gat aca tat gaa ata acg aag agt tat			585
His Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile Thr Lys Ser Tyr			
140	145	150	155
Taaattattc tgaatttgaa acaaaaaaaaaaaaahm			621

<210> 378
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 378
 Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val Leu Gln Leu Thr Thr
 20 -15 -10 -5
 Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val Asn Pro Phe Glu Xaa
 1 5 10
 Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala His His Phe Ile His
 15 20 25
 Pro Cys Leu Asp
 30

<210> 379
 <211> 193
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 379

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Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu Pro Pro Leu Xaa
      -20                      -15                      -10
Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro Glu Arg Gly Ala
      -5                      1                      5
Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg Phe Cys Pro Pro
10      15      20      25
Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp Lys Tyr Ser Asn
      30      35      40
Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu Ser Pro Leu Glu
      45      50      55
Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu Trp Asn Gln Gln
      60      65      70
Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu Lys Glu Glu Phe
      75      80      85
Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu Arg Thr Glu Ser
90      95      100      105
Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala Asp Phe Tyr Lys
      110      115      120
Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr Tyr Asn Arg Asp
      125      130      135
Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met Gly Lys Val Ala
      140      145      150
Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln Lys Lys Arg Ser
155      160      165

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Asn
170

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<210> 380
<211> 82
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -14...-1

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<400> 380
Met Ala Phe Thr Leu Xaa Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
      -10                      -5                      1
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
      5      10      15
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
      20      25      30
Lys Ser Xaa Xaa Met Xaa Leu Ile Arg Ser Val Arg Thr Val Met Arg
35      40      45      50
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
      55      60      65
Phe Gly

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<210> 381
<211> 198
<212> PRT
<213> Homo sapiens

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<220>
 <221> SIGNAL
 <222> -21...-1

<400> 381

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-20						-15					-10				
Arg	Pro	Ala	Ser	Ala	Ala	Pro	Met	Gly	Gly	Pro	Glu	Leu	Ala	Gln	His
-5				1				5						10	
Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu	Gln	Leu	Gly	Gln	Ala
			15					20					25		
Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Arg	Leu	Thr	Lys	Ala	Arg
		30				35						40			
Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu	Leu	Leu	Gly	Gln	Glu
45						50					55				
Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu	Leu	Arg	Ala	Ser	Leu	Leu
60					65					70					75
Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu	Xaa	Leu	Gln	Ala	Xaa	Ala	Thr
				80					85					90	
Ala	Glu	Val	Leu	Gly	Glu	Val	Ala	Gln	Ala	Gln	Lys	Val	Leu	Arg	Asp
			95					100					105		
Ser	Val	Gln	Arg	Leu	Xaa	Xaa	Gln	Leu	Xaa	Xaa	Ala	Trp	Leu	Gly	Pro
		110					115					120			
Ala	Tyr	Arg	Lys	Phe	Glu	Val	Leu	Lys	Ala	Pro	Pro	Xaa	Lys	Gln	Asn
	125						130				135				
His	Ile	Leu	Trp	Ala	Leu	Thr	Gly	His	Val	Xaa	Arg	Gln	Xaa	Arg	Glu
140					145					150					155
Met	Val	Ala	Gln	Gln	Xaa	Xaa	Leu	Xaa	Gln	Ile	Gln	Glu	Lys	Leu	His
				160					165					170	
Thr	Ala	Ala	Leu	Pro	Ala										
			175												

<210> 382
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55...-1

<400> 382

Met	Asp	Lys	Leu	Lys	Lys	Val	Leu	Ser	Gly	Gln	Asp	Thr	Glu	Asp	Arg
-55					-50					-45					-40
Ser	Gly	Leu	Ser	Glu	Val	Val	Glu	Ala	Ser	Ser	Leu	Ser	Trp	Ser	Thr
			-35						-30					-25	
Arg	Ile	Lys	Gly	Phe	Ile	Ala	Cys	Phe	Ala	Ile	Gly	Ile	Leu	Cys	Ser
		-20					-15						-10		
Leu	Leu	Gly	Thr	Val	Leu	Leu	Trp	Val	Pro	Arg	Lys	Gly	Leu	His	Leu
	-5						1				5				
Phe	Ala	Val	Phe	Tyr	Thr	Phe	Gly	Asn	Ile	Ala	Ser	Ile	Gly	Ser	Thr
10					15					20					25
Ile	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Arg	Met	Phe	Glu	Pro
				30					35					40	

Thr	Arg	Leu	Ile	Ala	Thr	Ile	Met	Val	Leu	Leu	Cys	Phe	Ala	Leu	Thr
			45					50					55		
Leu	Cys	Ser	Ala	Phe	Trp	Trp	His	Asn	Lys	Gly	Leu	Ala	Leu	Ile	Phe
		60					65					70			
Cys	Ile	Leu	Gln	Ser	Leu	Ala	Leu	Thr	Trp	Tyr	Ser	Leu	Ser	Phe	Ile
	75					80					85				
Pro	Phe	Ala	Arg	Asp	Ala	Val	Lys	Xaa	Cys	Phe	Ala	Val	Cys	Leu	Ala
90					95					100					105

<210> 383
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 383

Met	Lys	Ala	Leu	Cys	Leu	Leu	Leu	Leu	Pro	Val	Leu	Gly	Leu	Leu	Val
			-15					-10				-5			
Ser	Ser	Lys	Thr	Leu	Cys	Ser	Met	Glu	Glu	Ala	Ile	Asn	Glu	Arg	Ile
		1				5					10				
Gln	Glu	Val	Ala	Gly	Ser	Leu	Ile	Phe	Arg	Ala	Ile	Ser	Ser	Ile	Gly
15					20					25				30	
Arg	Gly	Ser	Glu	Ser	Val	Thr	Ser	Arg	Gly	Asp	Leu	Ala	Thr	Cys	Pro
				35					40					45	
Arg	Gly	Phe	Ala	Val	Thr	Gly	Cys	Thr	Cys	Gly	Ser	Ala	Cys	Gly	Ser
			50					55					60		
Trp	Asp	Val	Arg	Ala	Glu	Thr	Thr	Cys	His	Cys	Gln	Cys	Ala	Gly	Met
	65						70					75			
Asp	Trp	Thr	Gly	Ala	Arg	Cys	Cys	Arg	Val	Gln	Pro				
	80					85					90				

<210> 384
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 384

Met	Ile	Ser	Arg	Gln	Leu	Arg	Ser	Leu	Ser	Cys	Leu	Cys	Pro	Ala	Leu
		-20					-15					-10			
Phe	Pro	Gly	Thr	Ser	Ser	Phe	Ile	Val	Ala	Leu	Ser	Ser	Pro	Ala	Asp
	-5				1					5				10	
Leu	Tyr	Ile	Pro	Xaa	Arg	Xaa	Arg	Ser	Asp	Glu	Leu	Val	Phe	Glu	Ser
				15					20					25	
Gln	Lys	Gly	Ser	Ala	Met	Glu	Leu	Ala	Val	Ile	Thr	Val	Xaa	Gly	Val
				30				35						40	

<210> 385
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 385
 Met Gly Phe Leu Xaa Leu Met Thr Leu Thr Thr His Val His Ser Ser
 -15 -10 -5 1
 Ala Lys Pro Asn Glu Gln Pro Trp Leu Leu Asn
 5 10

<210> 386
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 386
 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 -20 -15 -10
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
 5 1 5 10
 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 15 20 25
 Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
 30 35 40
 Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
 45 50 55
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys
 60 65 70 75
 Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser
 80 85 90
 Pro Ser Thr Xaa Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu
 95 100 105
 Val Phe Met Arg Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly
 110 115 120
 Asn Xaa Gly Cys Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser
 125 130 135
 Ser Ser Pro Val Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile
 140 145 150 155
 Ile Ala Gly Glu Ser Ile Arg Asn Arg Ser
 160 165

<210> 387

<211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 387

```

Met Glu Thr Gly Ala Leu Arg Arg Pro Gln Leu Leu Pro Leu Leu Leu
  -25                      -20                      -15
Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys Arg Pro Val Leu Gln Asn
-10                      -5                      1                      5
Leu Leu Gln Ser Pro Gly Leu Thr Trp Ser Leu Glu Val Pro Thr Gly
          10                      15                      20
Arg Glu Gly Lys Glu Gly Gly Asp Arg Gly Pro Gly Leu Xaa Gly Ala
          25                      30                      35
Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu Met Gly Arg Gln Arg Thr
          40                      45                      50
Arg Lys Val Lys Gly Pro Ala Trp Xaa His Thr Ala Asn Gln Glu Leu
55                      60                      65                      70
Asn Arg Met Arg Ser Leu Ser Ser Gly Ser Val Pro Val Gly His Leu
          75                      80                      85
Glu Gly Gly Thr Val Lys Leu Gln Lys Asp Thr Gly Leu His Ser Cys
          90                      95                      100
Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr Pro Ala Ser Val Leu Ala
          105                      110                      115
Asp Ala Cys Pro Gly Phe His Asp Val Xaa Val Gln Xaa Ala Leu Phe
          120                      125                      130
Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys Thr His Phe Cys Leu Ser
135                      140                      145                      150
Ile Xaa Leu

```

<210> 388
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

<400> 388

```

Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys
-55                      -50                      -45                      -40
Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
          -35                      -30                      -25
Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr
          -20                      -15                      -10
Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met
          -5                      1                      5
Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly
10                      15                      20                      25
Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr
          30                      35                      40

```

```

Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
      45                      50                      55
Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala
      60                      65                      70
Pro Phe Pro Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser
      75                      80                      85
Pro Gly Cys Tyr Arg Tyr
90                      95

```

<210> 389
 <211> 236
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 389

```

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
-30                      -25                      -20
Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Ala Ala
15                      -10                      -5                      1
Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
      5                      10                      15
Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro Asp Leu
      20                      25                      30
Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln Ala Ser
35                      40                      45
Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Thr Pro Pro Ala Ala
50                      55                      60                      65
Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
      70                      75                      80
Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
      85                      90                      95
Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
100                      105                      110
Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu Gly Pro
115                      120                      125
Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe Glu Asp
130                      135                      140                      145
Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
      150                      155                      160
Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
      165                      170                      175
Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
180                      185                      190
Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
195                      200                      205

```

<210> 390
 <211> 149
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -100...-1

<400> 390

```

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
-100          -95          -90          -85
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
          -80          -75          -70
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile
          -65          -60          -55
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
          -50          -45          -40
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
          -35          -30          -25
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
-20          -15          -10          -5
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile
          1          5          10
Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
          15          20          25
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro
          30          35          40
Gly Tyr Leu Met Gly
45

```

<210> 391

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -49...-1

<400> 391

```

Met Pro Phe His Phe Pro Phe Leu Gly Phe Val Cys Leu His Leu His
          -45          -40          -35
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu
          -30          -25          -20
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Leu Ser Cys Val Gly
          -15          -10          -5
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His
          1          5          10          15
Phe Phe Ile Pro Asp
          20

```

<210> 392

<211> 241

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 392

Met	Gly	Thr	Ala	Ser	Arg	Ser	Asn	Ile	Ala	Arg	His	Leu	Gln	Thr	Asn
-30					-25					-20					-15
Leu	Ile	Leu	Phe	Cys	Val	Gly	Ala	Val	Gly	Ala	Cys	Thr	Leu	Ser	Val
				-10					-5					1	
Thr	Gln	Pro	Trp	Tyr	Leu	Glu	Val	Asp	Tyr	Thr	His	Glu	Ala	Val	Thr
	5					10					15				
Ile	Lys	Cys	Thr	Phe	Ser	Ala	Thr	Gly	Cys	Pro	Ser	Glu	Gln	Pro	Thr
20						25				30					
Cys	Leu	Trp	Phe	Arg	Tyr	Gly	Ala	His	Gln	Pro	Glu	Asn	Leu	Cys	Leu
35					40				45					50	
Asp	Gly	Cys	Lys	Ser	Glu	Ala	Xaa	Lys	Phe	Thr	Val	Arg	Glu	Ala	Leu
				55					60					65	
Lys	Glu	Asn	Gln	Val	Ser	Leu	Thr	Val	Asn	Arg	Val	Thr	Ser	Asn	Asp
			70					75					80		
Ser	Ala	Ile	Tyr	Ile	Cys	Gly	Ile	Ala	Phe	Pro	Ser	Val	Pro	Glu	Ala
		85					90					95			
Arg	Ala	Lys	Gln	Thr	Gly	Gly	Gly	Thr	Thr	Leu	Val	Val	Arg	Glu	Ile
100						105						110			
Lys	Leu	Leu	Ser	Lys	Glu	Leu	Arg	Ser	Phe	Leu	Thr	Ala	Leu	Val	Ser
115					120					125				130	
Leu	Leu	Ser	Val	Tyr	Val	Thr	Gly	Val	Cys	Val	Ala	Phe	Ile	Leu	Leu
				135					140					145	
Ser	Lys	Ser	Lys	Ser	Asn	Pro	Leu	Arg	Asn	Lys	Glu	Ile	Lys	Glu	Asp
			150					155					160		
Ser	Gln	Lys	Lys	Lys	Ser	Ala	Arg	Arg	Ile	Phe	Gln	Glu	Ile	Ala	Gln
		165					170					175			
Glu	Leu	Tyr	His	Lys	Arg	His	Val	Glu	Thr	Asn	Gln	Gln	Ser	Glu	Lys
180					185					190					
Asp	Asn	Asn	Thr	Tyr	Glu	Asn	Arg	Arg	Val	Leu	Ser	Asn	Tyr	Glu	Arg
195					200					205				210	
Pro															

<210> 393
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 393

Met	Asn	Cys	Asn	Val	Val	Ser	Glu	Arg	Gly	Lys	Trp	Leu	Glu	Val	Glu
-30					-25					-20					-15
Cys	Ser	Leu	Met	Thr	Cys	Thr	Thr	Leu	Ile	Asn	Ala	Ser	Ala	Ile	Ser
				-10					-5					1	
Thr	Asn	Thr	Leu	Thr	Asp	Met	Gly	Ser	Phe	Asp	Arg	Arg	Glu	Ser	
	5						10				15				

<210> 394
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 394
Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 -25 -20 -15
Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 -10 -5 1
Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
5 10 15 20
Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa
 25 30 35

Ser

<210> 395
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 395
Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu Pro
 -20 -15 -10
Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu Gly Lys
 -5 1 5
Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp Asp Ala Ala
10 15 20
Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa Asn Xaa Tyr Xaa Xaa
25 30 35 40
Trp Gly Gln Gly Thr His Ser Ser Leu
 45

<210> 396
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<400> 396

Met	Pro	Cys	Pro	Thr	Trp	Thr	Cys	Leu	Lys	Ser	Phe	Pro	Ser	Pro	Thr
			-15					-10					-5		
Ser	Ser	His	Ala	Ser	Ser	Leu	His	Leu	Pro	Pro	Ser	Cys	Thr	Arg	Leu
		1				5					10				
Thr	Leu	Thr	Gln	Thr	Leu	Arg	Thr	Gly	Met	His	Leu	Ser	Arg	Ala	Leu
15					20					25					30
Gln	Gly	Thr	Leu	Thr	Arg	Leu	Gln	Ser	Thr	Pro	Ala				
				35					40						

<210> 397
 <211> 192
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -93...-1

<400> 397

Met	Ala	Glu	Leu	Gly	Leu	Asn	Glu	His	His	Gln	Asn	Glu	Val	Ile	Asn
			-90					-85					-80		
Tyr	Met	Arg	Phe	Ala	Arg	Ser	Lys	Arg	Gly	Leu	Arg	Leu	Lys	Thr	Val
		-75					-70					-65			
Asp	Ser	Cys	Phe	Gln	Asp	Leu	Lys	Glu	Ser	Arg	Leu	Val	Glu	Asp	Thr
	-60					-55					-50				
Phe	Thr	Ile	Asp	Glu	Val	Ser	Glu	Val	Leu	Asn	Gly	Leu	Gln	Ala	Val
-45					-40					-35					-30
Val	His	Ser	Glu	Val	Glu	Ser	Glu	Leu	Ile	Asn	Thr	Ala	Tyr	Thr	Asn
				-25					-20					-15	
Val	Leu	Leu	Leu	Arg	Gln	Leu	Phe	Ala	Gln	Ala	Glu	Lys	Trp	Tyr	Leu
			-10				-5					1			
Lys	Leu	Gln	Thr	Asp	Ile	Ser	Glu	Leu	Glu	Asn	Arg	Glu	Leu	Leu	Glu
	5				10						15				
Gln	Xaa	Ala	Glu	Phe	Glu	Lys	Ala	Xaa	Ile	Thr	Ser	Ser	Asn	Lys	Lys
-20					25					30					35
Pro	Ile	Leu	Xaa	Val	Thr	Xaa	Pro	Lys	Leu	Ala	Pro	Leu	Asn	Glu	Gly
				40					45					50	
Gly	Thr	Ala	Lys	Leu	Leu	Asn	Lys	Val	Ile	Cys	Ile	Ile	Leu	Arg	Asn
			55					60					65		
Gly	Lys	Ser	Leu	Ile	Leu	Ser	Cys	His	Cys	Leu	Gly	Trp	Arg	Asn	Lys
		70					75					80			
Ser	Gly	Arg	Phe	Val	Ser	Gly	Pro	Leu	Arg	Ile	Ile	Ser	Pro	Leu	Gln
	85					90					95				

<210> 398
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -72...-1

<400> 398

```

Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
  -70                      -65                      -60
Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
  -55                      -50                      -45
Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
  -40                      -35                      -30                      -25
Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
                      -20                      -15                      -10
Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
                      -5                      1                      5
Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Ser Val
  10                      15                      20
Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala Pro Gly Pro Tyr
  25                      30                      35                      40
Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro Val Ala Pro Gln
                      45                      50                      55
His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn Gln Lys Thr Leu
                      60                      65                      70
Phe Ser Met Val Gly
  75

```

<210> 399

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 399

```

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
  -20                      -15                      -10                      -5
Leu Ala Gln Ala Leu Asp Cys His Val Cys Ala Tyr Asn Gly Asp Asn
                      1                      5                      10
Cys Phe Asn Pro Met Arg Cys Pro Ala Met Val Ala Tyr Cys Met Thr
                      15                      20                      25
Thr Arg Thr Tyr Tyr Thr Pro Thr Arg Met Lys Val Ser Lys Ser Cys
                      30                      35                      40
Val Pro Arg Cys Phe Glu Xaa Cys Val
  45                      50

```

<210> 400

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 400

[illegible]

<210> 401

<211> 78

<212> PRT

<213> Homo sapiens

<220>

=<221> SIGNAL

 $\langle 222 \rangle - 21 \dots -1$ $\leq 400 > 401$

Met	Cys	Pro	Val	Phe	Ser	Lys	Gln	Leu	Leu	Ala	Cys	Gly	Ser	Leu	Leu
	-20					-15					-10				
Pro	Gly	Leu	Trp	Gln	His	Leu	Thr	Ala	Asn	His	Trp	Pro	Pro	Phe	Ser
	5				1				5					10	
Xaa	Phe	Leu	Cys	Thr	Val	Cys	Ser	Gly	Ser	Ser	Glu	Gln	Ile	Ser	Glu
			15					20					25		
Tyr	Thr	Ala	Ser	Ala	Thr	Pro	Pro	Leu	Cys	Arg	Ser	Leu	Asn	Gln	Glu
		30					35					40			
Pro	Phe	Val	Ser	Arg	Ala	Ile	Arg	Pro	Lys	Tyr	Ser	Ile	Thr		
	45					50					55				

<210> 402

<211> 65

<212> PRT

<213> Homo sapiens

$\langle 220 \rangle$

<221> SIGNAL

<222> -28..-1

<400> 402

Met	Gly	Lys	Gly	His	Gln	Arg	Pro	Trp	Trp	Lys	Val	Leu	Pro	Leu	Ser
			-25					-20					-15		
Cys	Phe	Leu	Val	Ala	Leu	Ile	Ile	Trp	Cys	Tyr	Leu	Arg	Glu	Glu	Ser
		-10				-5					1				
Glu	Ala	Asp	Gln	Trp	Leu	Arg	Gln	Val	Trp	Gly	Glu	Val	Pro	Glu	Pro
5					10					15					20
Ser	Asp	Arg	Ser	Glu	Glu	Pro	Glu	Thr	Pro	Ala	Ala	Tyr	Arg	Ala	Arg
				25					30					35	

Thr

```
<210> 403
<211> 211
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> SIGNAL  
<222> -27..-1
```

<400> 403

[illegible]

Arg Ser Ile

```
<210> 404
<211> 123
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> -80..-1
```

<400> 404

Met Ser Thr Trp Tyr Leu Ala Leu Asn Lys Ser Tyr Lys Asn Lys Asp
-80 -75 -70 -65
Ser Val Arg Ile Tyr Leu Ser Leu Cys Thr Val Ser Ile Lys Phe Thr
-60 -55 -50

```

Tyr Phe His Asp Ile Gln Thr Asn Cys Leu Thr Thr Trp Lys His Ser
      -45                -40                -35
Arg Cys Arg Phe Tyr Trp Ala Phe Gly Gly Ser Ile Leu Gln His Ser
      -30                -25                -20
Val Asp Pro Leu Val Leu Phe Leu Ser Leu Ala Leu Leu Val Thr Pro
      -15                -10                -5
Thr Ser Thr Pro Ser Ala Lys Ile Gln Ser Leu Gln Ile Asp Leu Pro
1      5      10      15
Gly Gly Trp Arg Leu Ala Thr Asp Arg Ile Phe Thr Leu Ser Pro Val
      20      25      30
Pro Met Asp Xaa Pro Leu Ile Leu His Gln Leu
      35      40

```

<210> 405
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

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<400> 405
Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
      -25                -20                -15
Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
10      -5      1      5
Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu
      10      15      20
Ile Phe Ile Ser Ile Xaa Gly Ile Leu Tyr Lys Phe Xaa Asp Val Leu
      25      30      35
Leu Tyr Phe Pro Xaa Gln Xaa Ser Ser Ser Arg Leu Tyr Asp Ser His
      40      45      50
Ala His Trp Xaa Ser Xaa
55      60

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<210> 406
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

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<400> 406
Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu Ala Val Thr
      -30                -25                -20
Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro
      -15      -10      -5      1
Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys
      5      10      15
Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn

```


20	25	30
Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val		
35	40	45
Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn		
50	55	60
Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser		
	70	75
Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser His Val Ser		
	85	90
Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp Ile Pro Cys		
	100	105
Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp Asn Trp Glu		
	115	120
Pro Asn		125
130		

<210> 407

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 407

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile		
	-35	-30
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe		
	-20	-15
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu		
	5	1
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Xaa Gln		
	15	20
Xaa Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly		
	30	35
Gly Phe Ser Phe Cys Gln Xaa Arg Leu Asn Lys Arg Lys Glu Tyr Met		
	45	50
Val Arg		55
60		

<210> 408

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 408

Met Arg Phe Leu Pro Cys Cys Leu Leu Trp Ser Val Phe Asn Pro Glu		
-15	-10	-5
		1

Ser Leu Asn Cys His Tyr Phe Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser
5 10 15
Leu Gln Tyr Tyr Glu Ile Ser Leu Gln Glu Lys Leu Leu Gly Phe Leu
20 25 30
Trp Leu Cys Phe Leu Ser Tyr Phe Phe Arg Ala Val Tyr Phe Leu Ile
35 40 45
Asp Phe Ser Ser Phe Thr
50 55

<210> 409
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45...-1

<400> 409

Met His Ser Leu Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser
45 -40 -35 -30
Phe Ser Phe Arg Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly
-25 -20 -15
Glu Asn Phe Leu Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser
-10 -5 1
Gly Ser Thr Phe Met Arg Asp Ile Glu Thr Asn Lys
5 10 15

<210> 410
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22...-1

<400> 410

Met Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser
-20 -15 -10
Ser Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys
-5 1 5 10
Asn Pro Phe Leu Trp Lys Leu
15

<210> 411
<211> 51
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -23...-1

<400> 411

Met	Ala	Phe	Gln	Ser	Leu	Leu	Glu	Met	Lys	Phe	Phe	Leu	Cys	Ala	Ala
			-20					-15					-10		
Phe	Pro	Leu	Gly	Ala	Gly	Val	Lys	Met	Phe	His	Tyr	Leu	Gly	Pro	Gly
		-5					1				5				
Lys	Pro	Leu	Xaa	Gln	Ala	Ser	Pro	Ser	Pro	His	Pro	His	Arg	Xaa	Arg
10					15					20					25
Ile	Trp	Pro													

<210> 412
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -48...-1

<400> 412

Met	Ala	Ser	Ser	His	Trp	Asn	Glu	Thr	Thr	Thr	Ser	Val	Tyr	Gln	Tyr
			-45					-40					-35		
Leu	Gly	Phe	Gln	Val	Gln	Lys	Ile	Tyr	Pro	Phe	His	Asp	Asn	Trp	Asn
		-30					-25					-20			
Thr	Ala	Cys	Phe	Val	Ile	Leu	Leu	Leu	Phe	Ile	Phe	Thr	Val	Val	Ser
	-15					-10				-5					
Leu	Val	Val	Leu	Ala	Phe	Leu	Tyr	Glu	Val	Leu	Xaa	Xaa	Cys	Cys	Cys
				5				10					15		
Val	Lys	Asn	Lys	Thr	Val	Lys	Asp	Leu	Lys	Ser	Glu	Pro	Asn	Pro	Leu
		20					25					30			
Xaa	Xaa	Met	Met	Asp	Asn	Ile	Arg	Lys	Arg	Glu	Thr	Glu	Val	Val	
		35					40					45			

<210> 413
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32...-1

<400> 413

Met	Asp	Glu	Tyr	Ser	Trp	Trp	Cys	His	Val	Leu	Glu	Val	Val	Lys	Gly
		-30					-25					-20			
Gln	Met	Phe	Thr	Phe	Ile	Asn	Ile	Thr	Leu	Trp	Leu	Gly	Ser	Leu	Cys
	-15					-10					-5				
Gln	Arg	Phe	Phe	Tyr	Ala	Ser	Gly	Thr	Tyr	Phe	Leu	Ile	Tyr	Ile	Ser
1				5				10						15	
Thr	Val	Thr	Pro	Ser	Trp	Arg	Leu	Cys	Leu	Val	Ser				
			20					25							

<210> 414
 <211> 170
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -79..-1

<400> 414
 Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 -75 -70 -65
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 -60 -55 -50
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
 -45 -40 -35
 Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 -30 -25 -20
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 15 -10 -5 1
 Pro Ser Ser Lys Ala Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa
 5 10 15
 Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
 20 25 30
 Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa
 35 40 45
 Arg His Xaa Gln Xaa His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
 50 55 60 65
 Cys Thr Xaa Cys Gly Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln
 70 75 80
 His Tyr Ile Arg His Ala Arg Gly Gly Leu
 85 90

<210> 415
 <211> 190
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -82..-1

<400> 415
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe
 -80 -75 -70
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly
 -65 -60 -55
 Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val Ile
 -50 -45 -40 -35
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln
 -30 -25 -20
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr

			-15						-10						-5			
Trp	Gly	His	Ile	Ser	Trp	Asp	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Asp	Ile			
		1				5					10							
Ile	Leu	Ala	Ser	Asp	Val	Phe	Phe	Glu	Pro	Glu	Xaa	Phe	Glu	Asp	Ile			
15					20					25				30				
Leu	Ala	Thr	Ile	Tyr	Phe	Leu	Met	His	Lys	Asn	Pro	Lys	Val	Gln	Leu			
			35						40					45				
Trp	Ser	Thr	Tyr	Gln	Val	Arg	Xaa	Ala	Asp	Trp	Ser	Leu	Glu	Ala	Leu			
			50					55					60					
Leu	Tyr	Lys	Trp	Asp	Met	Lys	Cys	Val	His	Ile	Pro	Leu	Glu	Ser	Phe			
		65				70					75							
Asp	Ala	Asp	Lys	Glu	Xaa	Ile	Ala	Glu	Ser	Thr	Leu	Pro	Gly	Arg	His			
	80					85					90							
Thr	Val	Glu	Met	Leu	Val	Ile	Ser	Phe	Ala	Lys	Asp	Ser	Leu					
95					100					105								

<210> 416

<211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -60..-1

<400> 416

Met	Met	Ala	Ala	Val	Pro	Pro	Gly	Leu	Glu	Pro	Trp	Asn	Arg	Val	Arg			
60					-55				-50					-45				
Ile	Pro	Lys	Ala	Gly	Asn	Arg	Ser	Ala	Val	Thr	Val	Gln	Asn	Pro	Gly			
			-40					-35				-30						
Ala	Ala	Leu	Asp	Leu	Cys	Ile	Ala	Ala	Val	Ile	Lys	Glu	Cys	His	Leu			
		-25					-20					-15						
Val	Ile	Leu	Ser	Leu	Lys	Ser	Gln	Thr	Leu	Asp	Ala	Glu	Thr	Asp	Val			
	-10					-5					1							
Leu	Cys	Ala	Val	Leu	Tyr	Ser	Asn	His	Asn	Arg	Met	Gly	Arg	His	Lys			
5				10					15					20				
Pro	His	Leu	Ala	Leu	Lys	Gln	Val	Glu	Gln	Cys	Leu	Lys	Arg	Leu	Lys			
		25				30						35						
Asn	Met	Asn	Leu	Glu	Gly	Ser	Ile	Gln	Asp	Leu	Phe	Glu	Leu	Phe	Ser			
		40				45						50						

Ser Lys

<210> 417

<211> 161

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -108..-1

<400> 417

Met Thr Ser Gly Gln Ala Arg Ala Ser Xaa Gln Ser Pro Gln Ala Leu

	-105		-100		-95
Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser Ile Thr Leu Thr Leu					
-90		-85		-80	
Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg Asn Val Thr His Leu					
-75		-70		-65	
Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu Ser Gly Arg Glu Ala					
-60		-55		-50	-45
His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro Thr Ala Trp Ser Ser					
	-40		-35		-30
Asp Asp Cys Ala Leu His Gly His Cys Glu Gln Val Val Phe Thr Ala					
	-25		-20		-15
Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe Pro Ser Leu Tyr Ser					
	-10		-5		1
His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr Pro Arg Ser Gly Thr					
5		10		15	20
Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln Asn Thr Pro Lys Ile					
	25		30		35
Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu Glu Lys Ser Ile Met					
	40		45		50
Leu					

<210> 418
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 418
Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu
-20
-15
-10
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val
5
1
5
10
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val
15
20
25
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro
30
35
40
Leu Arg Met
45

<210> 419
 <211> 332
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 419
 Met Ile Xaa Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp

<213> Homo sapiens

<222> -19..-1

Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser Phe His
-15 -10 -5
Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser Arg His

		1					5					10					
His	Ile	Leu	Gln	Gln	Phe	Leu	Val	Arg	Lys	Ser	Val	Pro	Leu	Glu	Asn		
	15					20					25						
Ala	Ser	Leu	Pro	Phe	Pro	His	Leu	Gly	Ser	Ser	Leu	Phe	Lys	Ile	Val		
30					35					40					45		
Gly																	

<210> 421
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

Met	Pro	Thr	Gly	Lys	Gln	Leu	Ala	Asp	Ile	Gly	Tyr	Lys	Thr	Phe	Ser		
-30					-25					-20					-15		
Thr	Ser	Met	Met	Leu	Leu	Thr	Val	Tyr	Gly	Gly	Tyr	Leu	Cys	Ser	Val		
				-10					-5					1			
Arg	Val	Tyr	His	Tyr	Phe	Gln	Trp	Arg	Arg	Ala	Gln	Arg	Gln	Ala	Ala		
	5					10						15					
Glu	Glu	Gln	Lys	Xaa	Ser	Gly	Ile	Met									
20						25											

<210> 422
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

Met	Lys	Lys	Val	Leu	Leu	Leu	Ile	Thr	Ala	Ile	Leu	Ala	Val	Ala	Val		
	-15						-10					-5					
Gly	Phe	Pro	Val	Ser	Gln	Asp	Gln	Glu	Arg	Glu	Lys	Arg	Ser	Ile	Ser		
1				5			10							15			
Asp	Ser	Asp	Glu	Leu	Ala	Ser	Gly	Xaa	Phe	Val	Phe	Pro	Tyr	Pro	Tyr		
			20				25						30				
Pro	Phe	Arg	Pro	Leu	Pro	Pro	Ile	Pro	Phe	Pro	Arg	Phe	Pro	Trp	Phe		
		35					40					45					
Arg	Arg	Asn	Phe	Pro	Ile	Pro	Ile	Pro	Glu	Ser	Ala	Pro	Thr	Thr	Pro		
	50					55						60					
Leu	Pro	Ser	Glu	Lys													
65																	

<210> 423
 <211> 85

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17...-1

<400> 423
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 -15 -10 -5
Gly Phe Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser
 1 5 10 15
Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
 20 25 30
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
 35 40 45
Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
 50 55 60
Leu Pro Ser Glu Lys
 65

<210> 424
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 424
Met Thr Cys Arg Gly Ser Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser
 -25 -20 -15
Glu Leu Ser Leu Leu Pro Ser Ser Leu Trp Val Leu Ala Thr Ser Ser
 -10 -5 1
Pro Thr Ile Thr Ile Ala Leu Ala Met Ala Ala Gly Asn Leu Cys Pro
 5 10 15
Leu Pro Ser Ser Xaa Arg Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln
 20 25 30 35
Gln Xaa Ala Leu Leu
 40

<210> 425
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -56...-1

<400> 425
Met Val Pro Trp Pro Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile

-55		-50		-45
Ser Arg Phe Pro Phe Leu Pro Thr His Asp Pro Pro Thr Pro Ala His				
-40		-35		-30
Trp Ser Pro Ala Ser His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu				-25
	-20		-15	-10
Thr Leu Ala Leu Leu Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys				
	-5		1	5
Lys Leu Ala Gly Gln Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu				
10		15		20
Pro Leu Thr Leu Trp Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr				
25		30		35
Val Ala Gln Lys Lys Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro				40
	45		50	55
Val Pro Ser Trp Val Gln Phe Phe Leu Gly				
60		65		

<210> 426
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 426
Met Ala Cys Glu Thr His Gly Val Leu Val Pro Ala His Leu Ser Gly
30
-25
-20
-15
Leu Ile Thr Cys Leu Leu Ala Phe Trp Val Pro Ala Ser Cys Ile Gln
-10
-5
1
Arg Cys Ser Gly Ser Pro Leu Pro Leu
5
10

<210> 427
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 427
Met Ala Pro His Thr Ala Ser Phe Gly Val Cys Pro Leu Leu Ser Val
-35
-30
-25
Thr Arg Val Val Ala Thr Glu His Trp Leu Phe Leu Ala Ser Leu Ser
-20
-15
-10
-5
Gly Ile Lys Thr Tyr Gln Ser Tyr Ile Ser Val Phe Cys Lys Val Thr
1
5
10
Leu Ile

<210> 428
 <211> 136
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 428
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 -15 -10 -5
 Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 1 5 10
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 15 20 25 30
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
 35 40 45
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 50 55 60
 Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
 65 70 75
 Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
 80 85 90
 Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg Xaa Glu Asn Xaa
 95 100 105 110
 Met Pro Gly Leu Ser Gly Val Leu
 115

<210> 429
 <211> 194
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -65..-1

<400> 429
 Met Gln Asp Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser
 -65 -60 -55 -50
 Val Ser Ser Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr
 -45 -40 -35
 Arg Asn Leu Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys
 -30 -25 -20
 Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu
 -15 -10 -5
 Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala
 1 5 10 15
 Gly Leu Asp Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met
 20 25 30
 Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Ala Gln Thr Val Leu Asp
 35 40 45
 Asp Gly Ser Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp
 50 55 60

Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu	Asn	Asn	His	Cys	His	Val	Ala	Cys
65						70					75				
Ser	Ala	Leu	Xaa	Thr	Asp	Asp	Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Xaa
80					85				90						95
Lys	Ile	Val	Lys	Glu	Thr	Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys
				100					105					110	
Lys	His	Cys	Glu	Gly	Arg	Asp	Leu	Ser	Xaa	Trp	Lys	Lys	Gly	Cys	Glu
			115					120					125		
Val	Ser														

<210> 430
 <211> 141
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 430

Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
				-65					-60					-55	
Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			-50					-45					-40		
Gly	Gln	Asp	Ser	Leu	Lys	Lys	His	Leu	His	Ala	Glu	Ile	Lys	Val	Ile
		-35					-30					-25			
Gly	Thr	Ile	Gln	Ile	Leu	Cys	Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile
	-20					-15					-10				
Ile	Leu	Ala	Ser	Ala	Ser	Phe	Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser
-5					1				5					10	
Thr	Leu	Leu	Asn	Ser	Ala	Tyr	Pro	Phe	Ile	Gly	Pro	Phe	Phe	Val	Xaa
			15					20					25		
Lys	Xaa	Ser	Glu	Glu	Gly	Arg	Met	Gly	Gln	Xaa	Gly	Glu	Glu	Xaa	Xaa
		30					35					40			
Asn	Ser	Leu	Asn	Phe	Pro	Xaa	Ala	Ser	Leu	Leu	Xaa	Leu	Ile	Cys	Gln
	45					50					55				
Xaa	Gln	Gly	Phe	Asn	Gly	Glu	Ser	Cys	Ser	Pro	Val	Gly			
60					65					70					

<210> 431
 <211> 248
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 431

Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
				-65					-60					-55	
Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			-50					-45					-40		

Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Xaa Lys Val Ile
-35 -30 -25
Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
-20 -15 -10
Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
-5 1 5 10
Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile
15 20 25
Ile Ser Gly Ser Leu Ser Ile Ala Thr Lys Lys Arg Leu Thr Asn Leu
30 35 40
Leu Val His Thr Thr Leu Val Gly Ser Ile Leu Ser Ala Leu Ser Ala
45 50 55
Leu Val Gly Phe Ile Xaa Leu Ser Val Lys Gln Ala Thr Leu Asn Pro
60 65 70 75
Ala Ser Leu Xaa Cys Glu Leu Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa
80 85 90
Tyr Val Xaa Tyr Phe Tyr His Asp Ser Leu Tyr Thr Thr Asp Xaa Tyr
95 100 105
Thr Ala Lys Ala Xaa Leu Ala Gly Thr Leu Ser Leu Met Leu Ile Cys
110 115 120
Thr Leu Leu Glu Phe Cys Xaa Xaa Val Leu Thr Ala Val Leu Arg Trp
125 130 135
Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu Phe Leu Pro Xaa
140 145 150 155
Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met Thr His Asp Cys
160 165 170
Gly Tyr Glu Glu Leu Leu Thr Ser
175

<210> 432

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36..-1

<400> 432

Met Gln Val Pro His Leu Arg Val Trp Thr Gln Val Xaa Asp Thr Phe
-35 -30 -25
Ile Gly Tyr Arg Asn Leu Gly Phe Thr Ser Met Cys Ile Leu Phe His
-20 -15 -10 -5
Cys Leu Leu Ser Phe Gln Val Phe Lys Lys Lys Arg Lys Leu Xaa Leu
1 5 10
Phe

<210> 433

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL
<222> -14..-1

<400> 433

Met	Val	Ala	Leu	Asn	Leu	Ile	Leu	Val	Pro	Cys	Cys	Ala	Ala	Trp	Cys	
				-10					-5					1		
Asp	Pro	Arg	Arg	Ile	His	Ser	Gln	Asp	Asp	Val	Leu	Arg	Ser	Ser	Ala	
	5						10					15				
Ala	Asp	Thr	Gly	Ser	Ala	Met	Gln	Arg	Arg	Glu	Ala	Trp	Ala	Gly	Trp	
	20					25					30					
Arg	Arg	Ser	Gln	Pro	Phe	Ser	Val	Gly	Leu	Pro	Ser	Ala	Glu	Arg	Leu	
35					40					45					50	
Glu	Asn	Gln	Pro	Gly	Lys	Leu	Ser	Trp	Arg	Ser	Leu	Val	Gly	Glu	Gly	
				55					60					65		
His	Arg	Ile	Cys	Asp	Leu											
				70												

<210> 434

<211> 144

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -58..-1

<400> 434

Met	Thr	Arg	Leu	Cys	Leu	Pro	Arg	Pro	Glu	Ala	Arg	Glu	Asp	Pro	Ile	
			-55					-50					-45			
Pro	Val	Pro	Pro	Arg	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Ser	Gly	Ser	Pro	
	-40						-35					-30				
Val	Arg	Pro	Pro	Val	Ser	Thr	Trp	Gly	Pro	Ser	Trp	Ala	Gln	Leu	Leu	
	-25					-20					-15					
Asp	Ser	Val	Leu	Trp	Leu	Gly	Ala	Leu	Gly	Leu	Thr	Ile	Gln	Ala	Val	
10					-5					1				5		
Phe	Ser	Thr	Thr	Gly	Pro	Ala	Leu	Leu	Leu	Leu	Val	Ser	Phe	Leu		
			10				15					20				
Thr	Phe	Asp	Leu	Leu	His	Arg	Pro	Ala	Val	Thr	Leu	Cys	His	Ser	Ala	
	25					30						35				
Asn	Phe	Ser	Pro	Gly	Ala	Arg	Val	Arg	Gly	Pro	Val	Lys	Val	Leu	Asp	
	40					45					50					
Ser	Arg	Arg	Leu	Tyr	Ser	Cys	Lys	Trp	Val	Gln	Ser	Gln	Asp	Asn	Leu	
55					60					65				70		
Ala	Ser	Arg	Lys	His	Cys	Cys	Cys	Cys	Ser	Trp	Gly	Trp	Ala	Arg	Ser	
			75						80					85		

<210> 435

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16.,-1

<400> 435

Met	Glu	Arg	Leu	Val	Leu	Thr	Leu	Cys	Thr	Leu	Pro	Leu	Ala	Val	Ala
	-15					-10					-5				
Ser	Ala	Gly	Cys	Ala	Thr	Thr	Pro	Ala	Arg	Asn	Leu	Ser	Cys	Tyr	Gln
1				5					10					15	
Cys	Phe	Lys	Val	Ser	Ser	Trp	Thr	Glu	Cys	Pro	Pro	Thr	Trp	Cys	Ser
			20					25					30		
Pro	Leu	Asp	Gln	Val	Cys	Ile	Ser	Asn	Glu	Val	Val	Val	Ser	Phe	Ser
		35				40						45			
Glu	Ser	Pro	Pro	Gly	Arg	Gly	Xaa	Val	Pro	Xaa	Ala	Gly	Glu	Xaa	Pro
		50				55					60				
Val	Pro	Pro	Pro	Leu	Xaa	Asp	Leu	Xaa	Met	Thr	Pro	Arg	Xaa	Xaa	Arg
65					70					75					80
Ala	Trp	Gly	Pro	Val	Gly	Pro	Lys	Val	Pro	Pro	Ala	Val	Ser	Pro	Ala
				85					90					95	
Leu	Gly	Ser	Gly	Glu	His	Pro	Xaa	Xaa							
			100					105							

$\chi_{210} = 436$

$\langle 211 \rangle$ 162

<212> PRT

213 Homo sapiens

 $\Sigma < 220 >$

..K221> SIGNAL

 $\langle 222 \rangle$ -16..-1

„<400> 436

[illegible]

<210> 437
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 437

Met	Xaa	Leu	Met	Val	Leu	Val	Phe	Thr	Ile	Gly	Leu	Thr	Leu	Leu	Leu
-20					-15					-10					-5
Gly	Xaa	Gln	Ala	Met	Pro	Ala	Asn	Arg	Leu	Ser	Cys	Tyr	Arg	Lys	Ile
			1				5						10		
Leu	Lys	Asp	His	Asn	Cys	His	Asn	Leu	Pro	Glu	Gly	Val	Ala	Asp	Leu
	15						20					25			
Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp	Asp	Gly	Lys	Gly
	30					35					40				
Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Lys	Arg	Ile	Ala	Leu	Leu	Pro
45					50					55					60
Lys	Arg	Arg	Phe	Leu	Trp	Thr	Lys	Asp	Leu	Phe	Arg	Asp	Ser	Leu	Gln
			65						70					75	
Gln	Ser	Met	Arg	Ile	Phe	Met	Tyr	Ser	Gly	Glu	His	His	Ser		
			80					85					90		

<210> 438
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 438

Met	Lys	Leu	Leu	Thr	His	Asn	Leu	Leu	Ser	Ser	His	Val	Arg	Gly	Val
-15					-10					-5					1
Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala	Thr	Glu	Val	Arg	Ile
		5						10				15			
Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala	Arg	Met	Ile	Pro	Lys
		20					25					30			
Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Xaa	Asp	Asn	Leu	Arg	Leu	Ile
	35					40					45				
Gln	Val	Pro	Arg	Arg	Ala	Gly									
50						55									

<210> 439
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -24...-1

<400> 439

Met	Lys	Ser	Ala	Lys	Leu	Gly	Phe	Leu	Leu	Arg	Phe	Phe	Ile	Phe	Cys
				-20					-15					-10	
Ser	Leu	Asn	Thr	Leu	Leu	Leu	Gly	Gly	Val	Asn	Lys	Ile	Ala	Glu	Lys
			-5				1				5				
Ile	Cys	Gly	Asp	Leu	Lys	Asp	Pro	Cys	Lys	Leu	Asp	Met	Asn	Phe	Gly
10					15					20					
Ser	Cys	Tyr	Glu	Val	His	Phe	Arg	Tyr	Phe	Tyr	Asn	Arg	Thr	Ser	Lys
25					30				35					40	
Arg	Cys	Glu	Thr	Phe	Val	Phe	Ser	Ser	Cys	Asn	Gly	Asn	Leu	Asn	Asn
				45					50					55	
Phe	Lys	Leu	Lys	Ile	Glu	Arg	Glu	Val	Xaa	Cys	Val	Ala	Lys	Tyr	Lys
			60					65					70		
Pro	Pro	Arg													
			75												

<210> 440

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 440

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu
25				-20					-15					-10	
Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser
				-5				1				5			
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Gln	Arg	Phe	Phe	Ala
10						15					20				
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala
25					30					35					
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu
40					45					50				55	
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr
				60					65					70	
Ala	Ser	Trp	Phe	Glu	Ser	Phe	Cys	Gln	Phe	Thr	His	Tyr	Arg	Cys	Ser
			75					80					85		
Asn	His	Val	Tyr	Tyr	Ala	Lys	Arg	Val	Leu	Cys	Ser	Gln	Pro	Val	Ser
		90				95					100				
Ile	Leu	Ser	Pro	Asn	Thr	Leu	Lys	Glu	Ile	Glu	Xaa	Ser	Ala	Glu	Val
105						110					115				
Ser	Pro	Thr	Thr	Asp	Asp	Leu	Pro	His	Leu	Thr	Pro	Leu	His	Ser	Asp
120					125					130					135
Arg	Thr	Pro	Asp	Leu	Pro	Ala	Leu	Ala							
				140											

<210> 441

<211> 167

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -76..-1

<400> 441

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Met Gly Asp Tyr Leu Leu Arg Gly Tyr Arg Met Leu Gly Glu Thr Cys
-75                      -70                      -65
Ala Asp Cys Gly Thr Ile Leu Leu Gln Asp Lys Gln Arg Lys Ile Tyr
-60                      -55                      -50                      -45
Cys Val Ala Cys Gln Glu Leu Asp Ser Asp Val Asp Lys Asp Asn Pro
                      -40                      -35                      -30
Ala Leu Asn Ala Gln Ala Ala Leu Ser Gln Ala Arg Glu His Gln Leu
                      -25                      -20                      -15
Ala Ser Ala Ser Glu Leu Pro Leu Gly Ser Arg Pro Ala Pro Gln Pro
                      -10                      -5                      1
Pro Val Pro Arg Pro Glu His Cys Glu Gly Ala Ala Ala Gly Leu Lys
5                      10                      15                      20
Ala Ala Gln Gly Pro Pro Ala Pro Ala Val Pro Pro Asn Thr Xaa Val
                      25                      30                      35
Met Ala Cys Thr Gln Thr Ala Leu Leu Gln Lys Leu Thr Trp Ala Ser
                      40                      45                      50
Ala Glu Leu Gly Ser Xaa Thr Ser Xaa Gly Lys Xaa Ala Ser Ser Cys
                      55                      60                      65
Val Ala Leu Ser Ala His Val Arg Arg Pro Cys Ala Ala Cys Ser Ser
                      70                      75                      80
Tyr Ser Thr Lys Arg Ser Pro
85                      90

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<210> 442

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 442

```

Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
-15                      -10                      -5                      1
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
                      5                      10                      15
Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys Xaa Arg Thr Lys Tyr Glu
                      20                      25                      30
Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly Gly Asn Xaa Xaa Xaa Xaa
                      35                      40                      45
Xaa Leu Ser Lys Arg Asp
50                      55

```

<210> 443

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<220>
<221> SIGNAL
<222> -33..-1
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<400> 443

Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln	Arg	Val	Ser	Ser
			-30					-25					-20		
Val	Gly	Ala	Asn	Xaa	Leu	Cys	Leu	Gly	Met	Ala	Leu	Cys	Pro	Arg	Gln
		-15					-10					-5			
Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser
1				5					10					15	
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu
			20					25						30	
Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val
		35					40					45			
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu
	50						55				60				
Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Xaa	Lys	Leu	Lys	Gly	Glu	Thr	Met
65						70					75				
Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	Asn	Ile	Val	Cys
80					85					90					95
Ser	Lys	Xaa	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	Val	Ile	Ile	Thr
			100					105						110	
Ala	Gly	Ala	Arg	Gln	Xaa	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Leu	Xaa	Gln
		115					120					125			
Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	Ile	Val	Gln	Tyr
	130						135					140			
Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu
	145					150					155				
Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile
160					165					170					175
Gly	Ser	Gly	Cys	Asn	Leu	Ile	Xaa	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly
			180					185						190	
Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly
		195						200				205			
Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala
	210						215					220			
Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp
	225					230					235				
Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr
240					245					250					255
Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly	Leu	Ser
			260						265					270	
Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Arg	Ile	His
		275						280				285			
Pro	Val	Ser	Thr	Ile	Thr	Lys	Gly	Leu	Tyr	Gly	Ile	Xaa	Glu	Glu	Val
		290					295					300			
Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly	Ile	Thr	Asn	Leu
	305					310					315				
Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu							

<210> 444
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 444
 Met Tyr Tyr Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His
 -10 -5 1
 Leu Pro Ile Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr
 5 10 15
 Val Tyr Pro Thr Ser Ala Gly
 20 25

<210> 445
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37...-1

<400> 445
 Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 -35 -30 -25
 Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 -20 -15 -10
 Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met Pro
 5 1 5 10
 Asp Asn

<210> 446
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 446
 Met Thr Pro Trp Cys Leu Ala Cys Leu Gly Arg Arg Pro Leu Ala Ser
 -25 -20 -15
 Leu Gln Trp Ser Leu Thr Leu Ala Trp Cys Gly Ser Gly Ser His Trp
 -10 -5 1 5
 Thr Glu Arg Pro Xaa Gln Xaa Ser Pro Trp Xaa Ser Leu Ser Ala Thr

10 15 20
 Thr Arg Gly
 25

<210> 447
 <211> 242
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 447

Met	Gly	Glu	Ala	Ser	Pro	Pro	Ala	Pro	Ala	Arg	Arg	His	Leu	Leu	Val
-30					-25					-20					-15
Leu	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Val	Ile	Pro	Ser	Ala	Ala	Ala	Pro
				-10					-5					1	
Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	Leu	Thr	Gly	Leu
	5					10					15				
Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	Lys	Gly	Asn	Leu
	20				25					30					
Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	Asp	Phe	Arg	Gly
	35				40				45					50	
Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	His	Gln	Leu	Gly
			55					60					65		
Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	Met	Thr	Asp	Asn
		70					75					80			
Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Asn	Val	Val	Ala	Ser	Ile	Gln
	85					90					95				
Pro	Xaa	Glu	Gly	Xaa	Phe	Glu	Gly	Asp	Leu	Lys	Val	Pro	Arg	Met	Glu
	100					105					110				
Glu	Lys	Glu	Ala	Leu	Val	Pro	Xaa	Gln	Lys	Ala	Thr	Asp	Ser	Phe	His
	115				120					125					130
Thr	Glu	Leu	His	Pro	Arg	Val	Ala	Phe	Trp	Ile	Ile	Lys	Leu	Pro	Arg
			135					140					145		
Arg	Arg	Ser	His	Gln	Asp	Ala	Leu	Glu	Gly	Gly	His	Trp	Leu	Xaa	Glu
		150					155					160			
Lys	Arg	His	Arg	Leu	Gln	Ala	Ile	Arg	Asp	Gly	Leu	Arg	Lys	Gly	Thr
	165					170					175				
His	Lys	Asp	Xaa	Leu	Xaa	Xaa	Gly	Thr	Glu	Ser	Ser	Ser	His	Ser	Arg
	180				185					190					
Leu	Ser	Pro	Arg	Lys	Xaa	His	Leu	Leu	Tyr	Ile	Leu	Xaa	Pro	Ser	Arg
	195			200					205					210	
Gln	Leu														

<210> 448
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -60..-1

<400> 448

[illegible]

210 449

 $\lambda_{211} > 89$

212> PRT

213> Homo sapiens

 $\langle 220 \rangle$

<221> SIGNAL

 $\langle 222 \rangle$ -61...-1

400 > 449

[illegible]

<210> 450

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL
<222> -26...-1

<400> 450
Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
-25 -20 -15
Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
-10 -5 1 5
Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
10 15 20
Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly
25 30 35
Phe Asp Leu Asp Met Asp His Thr Ile
40 45

<210> 451
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34...-1

<400> 451
Met Ile Pro Leu Ile Ser His Leu Ala Glu Ala Ala Pro Pro Thr Ser
-30 -25 -20
Trp Ser Leu Ile Ser Ser Val Leu Asn Val Gly His Leu Leu Phe Ser
-15 -10 -5
Ser Ala Cys Ser Val Ser Leu Glu Ala Leu Ser Thr Arg Asn Ile Lys
1 5 10
Ala Ile Ile Leu Met Lys
15 20

<210> 452
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38...-1

<400> 452
Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
-35 -30 -25
Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
-20 -15 -10
Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
-5 1 5 10
Phe Lys Thr Ala Phe Gln Leu Leu Asp Phe Ile Leu Ala Val Leu Trp
15 20 25
Ala Val Val Trp Phe Met Gly Phe Cys Phe Leu Ala Asn Gln Trp Gln

[illegible]

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<210> 453
<211> 166
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -37..-1
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[illegible]

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<210> 454
<211> 180
<212> PRT
<213> Homo sapiens
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```
<220>  
<221> SIGNAL  
<222> -26..-1
```

<400> 454
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15


```

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10          -5          1          5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
          10          15          20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
          25          30          35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
          40          45          50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55          60          65          70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
          75          80          85
Val Xaa Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
          90          95          100
Gly Lys Met Ser Xaa Tyr Leu Asp Xaa Leu Lys Val Gly Asp Xaa Val
          105          110          115
Glu Phe Xaa Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
          120          125          130
Phe Asn Ile Gln Pro Asn Lys Asn Leu His Gln Asn Pro Glu Trp Arg
135          140          145          150
Arg Asn Trp Glu

```

<210> 455

<211> 91

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -64...-1

<400> 455

```

Met Thr Pro Arg Ile Leu Ser Glu Val Gln Phe Ser Ala Phe Cys Pro
          -60          -55          -50
Tyr Trp Thr Ile Ala Arg Ile Leu Glu Arg Val Gly Ser Ala Cys Phe
          -45          -40          -35
Arg Leu Glu Leu Cys Ala Ala Ile Val Gly Tyr Phe Val Leu Asp Val
          -30          -25          -20
Arg Thr Phe Leu Phe Ile Val Val Cys Val Ile Cys Val Thr Leu Asn
          -15          -10          -5
Phe Pro Arg Phe Tyr Phe Leu Cys Leu Ser Ser Leu Thr Ala Phe Gly
1          5          10          15
Thr Pro Pro Ile Gly Val His Ile Pro Ser Pro
          20          25

```

<210> 456

<211> 257

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 456

```

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
-20 -15 -10
Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
-5 1 5
Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
10 15 20 25
Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
30 35 40
Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
45 50 55
Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
60 65 70
Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
75 80 85
Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Xaa Xaa Phe Cys Gln Arg
90 95 100 105
Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Ala Thr Asn Gly
110 115 120
Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
125 130 135
Asn His Glu Ala Ser Xaa Ile Lys Glu Thr Trp Lys Lys Asp Arg Xaa
140 145 150
Leu Glu Xaa Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
155 160 165
Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Xaa Pro Xaa Val
170 175 180 185
Ser Pro Xaa Asn Ala Ser Xaa Ile His Trp Ser Ser Ser Xaa Leu Pro
190 195 200
Xaa Xaa Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Xaa Leu Met Gly
205 210 215
Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Xaa Xaa Ser Thr Xaa
220 225 230
Xaa

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<210> 457

<211> 193

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -60...-1

<400> 457

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Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
-60 -55 -50 -45
Cys Ser Gly Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
-40 -35 -30
Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
-25 -20 -15
Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
-10 -5 1
Leu Gly Ser Cys Gly Trp Xaa Cys His Thr Ala Gln Val Pro Ala Pro

```

5					10					15					20
Leu	Gln	Leu	Pro	Thr	Ala	Cys	Pro	Pro	Leu	Pro	His	Gly	Thr	Arg	Ala
				25					30					35	
Val	Gly	Pro	Thr	Pro	Gly	Leu	Leu	Pro	Glu	Ala	Ala	Ala	Pro	Xaa	Thr
			40					45					50		
Xaa	Gly	Ala	Leu	Ser	Ser	Arg	Ser	Arg	His	Trp	Ser	Cys	Ser	Ile	Val
		55					60					65			
Xaa	Cys	Leu	His	Leu	His	Xaa	Leu	Leu	Ser	Val	Glu	Thr	Arg	Xaa	Phe
	70					75				80					
Xaa	Lys	His	Leu	Leu	Val	Leu	Leu	Val	Ala	Val	Ala	His	Ser	Val	Leu
85					90				95					100	
Glu	Pro	Pro	Ala	Leu	Val	Pro	Asn	Val	Gln	Cys	Glu	Met	Cys	Thr	His
			105					110						115	
Ser	Gly	Pro	Arg	Asp	Leu	Glu	Ala	Ala	Val	Val	Ser	Pro	Ala	Pro	Trp
			120					125					130		
Glu															

<210> 458
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 458															
Met	Val	Leu	Thr	Leu	Gly	Glu	Ser	Trp	Pro	Val	Leu	Val	Gly	Arg	Arg
			-25					-20					-15		
Phe	Leu	Ser	Leu	Ser	Ala	Ala	Asp	Gly	Ser	Asp	Gly	Ser	His	Asp	Ser
		-10					-5				1				
Trp	Asp	Val	Glu	Arg	Val	Ala	Glu	Trp	Pro	Trp	Leu	Ser	Gly	Thr	Ile
					10					15				20	
Arg	Ala	Val	Ser	His	Thr	Asp	Val	Thr	Lys	Lys	Asp	Leu	Lys	Val	Cys
				25				30					35		
Val	Glu	Phe	Xaa	Gly	Glu	Ser	Trp	Arg	Lys	Arg	Arg	Trp	Ile	Glu	Val
		40					45					50			
Tyr	Ser	Leu	Leu	Arg	Lys	Ala	Phe	Leu	Val	Lys	His	Asn	Leu	Val	Leu
		55				60					65				
Ala	Glu	Arg	Lys	Ser	Pro	Glu	Ile	Ser	Trp	Gly					
	70					75									

<210> 459
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 459
 Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr

```

      -10      -5      1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
  5          10      15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20          25      30      35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala Gln Leu Arg Thr
      40      45      50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Xaa Phe Gly Gly Arg
      55      60      65
Met Xaa Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
      70      75      80
Thr Glu Phe Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
      85      90      95
Phe Leu Ile Pro Asn Leu Ala Leu Asn
100          105

```

<210> 460

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 460

```

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
      -15      -10      -5
Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
  1          5      10      15
Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Ile
      20      25

```

<210> 461

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13..-1

<400> 461

```

Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys
      -10      -5      1
Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro
  5          10      15
Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro
20          25      30      35
Thr Val Tyr Ser Ser Ala Pro Phe His Ala Pro Leu Pro Val Gln Asn
      40      45      50
Ser Leu Trp Gly His Pro Leu His Gly Cys Ser Trp Gln Cys His His
      55      60      65

```

Pro	Gln	Gly	Gln	Asn	Leu	Gln	Pro	Ala	Ser	Leu	Xaa	Thr	His	Leu	Ser
		70					75					80			
Lys	Pro	Lys	Arg	His	Phe	Xaa	Lys	Lys	Xaa	Cys	Gln	Ala			
	85					90					95				

<210> 462
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

Met	Ala	Thr	Ala	Thr	Glu	Gln	Trp	Val	Leu	Val	Glu	Met	Val	Gln	Ala
	-40					-35					-30				
Leu	Tyr	Glu	Ala	Pro	Ala	Tyr	His	Leu	Ile	Leu	Glu	Gly	Ile	Leu	Ile
	-25				-20					-15					-10
Leu	Trp	Ile	Ile	Arg	Leu	Leu	Phe	Ser	Lys	Thr	Tyr	Lys	Leu	Gln	Glu
				-5					1			5			
Arg	Ser	Asp	Leu	Thr	Val	Lys	Glu	Lys	Glu	Glu	Leu	Ile	Glu	Glu	Trp
		10				15					20				
Gln	Pro	Glu	Pro	Leu	Val	Pro	Pro	Val	Pro	Lys	Asp	His	Pro	Ala	Leu
	25					30					35				
Asn	Tyr	Asn	Ile	Val	Ser	Gly	Pro	Pro	Ser	His	Lys	Thr	Val	Val	Asn
	40				45				50						55
Gly	Lys	Glu	Cys	Ile	Asn	Phe	Ala	Ser	Phe	Asn	Phe	Leu	Gly	Leu	Leu
				60					65				70		
Asp	Asn	Pro	Arg	Val	Lys	Ala	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Lys	Tyr
			75					80				85			
Gly	Val	Gly	Thr	Cys	Gly	Pro	Cys	Gly	Phe	Tyr	Gly	Thr	Phe	Glu	
		90					95					100			

<210> 463
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

Met	Ala	Ala	Thr	Ser	Gly	Thr	Asp	Glu	Pro	Val	Ser	Gly	Glu	Leu	Val
	-30				-25					-20					-15
Ser	Val	Ala	His	Ala	Leu	Ser	Leu	Pro	Ala	Glu	Ser	Tyr	Gly	Asn	Xaa
			-10						-5				1		
Xaa	Asp	Ile	Glu	Met	Ala	Trp	Ala	Met	Arg	Ala	Met	Gln	His	Ala	Glu
	5						10					15			
Val	Tyr	Tyr	Lys	Leu	Ile	Ser	Ser	Val	Asp	Pro	Gln	Phe	Leu	Lys	Leu
	20					25					30				
Thr	Lys	Val	Asp	Asp	Gln	Ile	Tyr	Ser	Glu	Phe	Arg	Lys	Asn	Phe	Glu

35 40 45 50
Thr Leu Arg Ile Asp Val Leu Xaa Pro Glu Xaa Leu Lys Ser Glu Ser
55 60 65
Ala Lys Glu Pro Pro Gly Tyr Asn Ser Leu Pro Leu Lys Leu Leu Gly
70 75 80
Thr Gly Lys Ala Ile Thr Lys Leu Phe Ile Ser Val Phe Arg Thr Lys
85 90 95
Lys Glu Arg Lys Glu Ser Thr Met Glu Glu Lys Lys Glu Leu Thr Val
100 105 110
Glu Lys Lys Arg Thr Pro Arg Met Glu Glu Arg Lys Glu Leu Ile Val
115 120 125 130
Glu Lys Lys Lys Arg Lys Glu Ser Thr Glu Lys Thr Lys Leu Thr Lys
135 140 145
Glu Glu Lys Lys Gly Lys Lys Leu Thr Lys Lys Ser Thr Lys Val Val
150 155 160
Lys Lys Leu Cys Lys Val Tyr Arg Glu Gln His Ser Arg Ser Tyr Asp
165 170 175
Ser Ile Glu Thr Thr Ser Thr Thr Val Leu Leu Ala Gln Thr Pro Leu
180 185 190
Val Lys Cys Lys Phe Leu Tyr Asn
195 200

<210> 464
<211> 61
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -21...-1

<400> 464
Met Thr Phe Arg His Gln Asp Asn Ser Leu Met Phe Phe Ser Met Met
-20 -15 -10
Ala Thr Cys Thr Ser Asn Val Gly Phe Thr His Thr Thr Met Asn Cys
5 1 5 10
Ser Leu Thr Ser Pro Val Asp Phe Lys Asp Leu Leu Arg Val Leu Leu
15 20 25
Ile Lys Phe Gly Tyr Asp Arg Lys Ser Thr Ile Lys Ser
30 35 40

<210> 465
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19...-1

<400> 465
Met Phe Leu Lys Ser Gly Ala Gly Leu Ser Ser Cys Leu Leu Pro Leu
-15 -10 -5

Cys Trp Leu Glu Arg Lys Asp His Gly Arg Arg Pro Ser Xaa His Pro
1 5 10
Gly Arg
15

<210> 466
<211> 215
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -54..-1

<400> 466
Met Asn Xaa Tyr Ala Ser Pro Phe Asn Xaa Gln Leu Xaa Tyr Leu Xaa
-50 -45 -40
Leu Ser Arg Phe Glu Cys Val His Arg Asp Gly Arg Val Ile Thr Leu
-35 -30 -25
Ser Tyr Gln Glu Gln Glu Leu Gln Asp Phe Leu Leu Ser Gln Met Ser
-20 -15 -10
Gln His Gln Val His Ala Val Gln Gln Leu Ala Lys Val Met Gly Trp
-5 1 5 10
Gln Val Leu Ser Phe Ser Asn His Val Gly Leu Gly Pro Ile Glu Ser
15 20 25
Xaa Gly Asn Ala Ser Ala Ile Thr Val Ala Pro Gln Val Val Thr Met
30 35 40
Leu Phe Gln Phe Val Met Asp Leu Lys Val Ala Ala Arg Leu Trp Phe
45 50 55
Ser Phe Leu Val Thr Asn Val Lys Thr Phe Gln Lys Val Met Phe Tyr
60 65 70
Lys Ile Thr Asn Gly Val Ile Phe Val Gly His Ser Lys Lys Phe Ser
75 80 85 90
Gly Ile Lys Trp Lys Val Xaa Ile Leu Phe Ile Lys Trp Xaa Cys Leu
95 100 105
Cys Leu His Leu Ala Leu Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro
110 115 120
Lys Xaa Val Ser Xaa Asn Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr
125 130 135
Lys His Lys Glu Glu Ile Thr Ser Lys Arg Val Leu Phe Leu Lys Ile
140 145 150
Ile Ile Arg Lys Cys Phe Ile
155 160

<210> 467
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 467

Met Val Val His Leu Leu Tyr Ala His Leu Ser Phe Thr Ser Lys Arg
 -15 -10 -5
 Ala Val Val Met Leu Lys Leu Glu Ile Thr Phe
 1 5 10

<210> 468

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 468

Met Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu
 -20 -15 -10
 Phe Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys
 -5 1 5
 Phe Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser
 10 15 20
 Leu Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe
 25 30 35 40
 Pro Ser Thr Cys Asn Cys Phe Cys Tyr Leu Thr Ile Ile Ala Leu Xaa
 45 50 55
 Tyr Trp Asp Asn Leu
 60

<210> 469

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 469

Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala
 -15 -10 -5
 Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu
 1 5 10 15
 Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu
 20 25 30
 Pro Asn Phe
 35

<210> 470

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -43...-1

<400> 470

Met	Thr	Pro	Gln	Tyr	Leu	Pro	His	Gly	Gly	Lys	Tyr	Gln	Val	Leu	Gly
			-40					-35					-30		
Asp	Tyr	Ser	Leu	Ala	Val	Val	Phe	Pro	Leu	His	Phe	Ser	Asp	Leu	Ile
		-25					-20				-15				
Ser	Val	Leu	Tyr	Leu	Ile	Pro	Lys	Thr	Leu	Thr	Thr	Asn	Thr	Ala	Val
	-10				-5					1				5	
Lys	His	Ser	Ile	Gln	Lys	Asn	Cys	Met	Xaa	Leu	Val	Leu	Gly	Lys	Leu
			10					15					20		
Leu	Ser	Gln													

<210> 471

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 471

Met	Gly	Ile	Leu	Ser	Thr	Val	Thr	Ala	Leu	Thr	Phe	Ala	Arg	Ala	Leu
-15					-10				-5						1
Asp	Gly	Cys	Arg	Asn	Gly	Ile	Ala	His	Pro	Ala	Ser	Glu	Lys	His	Arg
		5					10					15			
Leu	Glu	Lys	Cys	Arg	Glu	Leu	Glu	Ser	Ser	His	Ser	Ala	Pro	Gly	Ser
	20				25						30				
Thr	Gln	His	Arg	Arg	Lys	Thr	Arg	Arg	Asn	Tyr	Ser	Ser	Ala		
35					40				45						

<210> 472

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -58...-1

<400> 472

Met	Ser	Thr	Gly	Gln	Leu	Tyr	Arg	Met	Glu	Asp	Ile	Gly	Arg	Phe	His
			-55					-50					-45		
Ser	Gln	Gln	Pro	Gly	Ser	Leu	Thr	Pro	Ser	Ser	Pro	Thr	Val	Gly	Glu
	-40					-35					-30				
Ile	Ile	Tyr	Asn	Asn	Thr	Arg	Asn	Thr	Leu	Gly	Trp	Ile	Gly	Gly	Ile
-25					-20					-15					
Leu	Met	Gly	Ser	Phe	Gln	Gly	Thr	Ile	Ala	Gly	Gln	Gly	Thr	Gly	Ala

-10					-5				1				5		
Thr	Ser	Ile	Ser	Glu	Leu	Cys	Lys	Gly	Gln	Glu	Leu	Glu	Pro	Ser	Gly
			10					15					20		
Ala	Gly	Leu	Thr	Val	Ala	Pro	Pro	Gln	Ala	Val	Ser	Leu	Gln	Gly	Ile
		25					30					35			
Tyr	Thr	Leu	Pro	Trp	Leu	Leu	Gln	Leu	Phe	His	Ser	Thr	Ala	Leu	Xaa
	40				45					50					
Xaa	Xaa	Gln	Gln	Pro	Asn	Gly	Ser	Leu	Ser	Leu	Asn	Ile	Ser	Ser	Ser
55					60					65				70	
His	Ala	Pro	Xaa	Pro	Xaa	Thr	Cys	Thr	Leu	Glu	Pro	Gly	Val	Asp	Pro
				75				80					85		
Thr	Arg	Xaa	Val	Cys	Ile	Asn	Pro	His	Pro	Pro	Pro	Pro	Ile	Leu	Lys
			90				95						100		
Xaa	Pro	Leu	Ser	Pro	Tyr	Pro	Lys	Pro	Gln	Leu	Gly	Thr	His	Ala	Gly
		105					110					115			
Gln	Val	Asn													
		120													

<210> 473

<211> 238

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -71...-1

<400> 473

Met	Xaa	Xaa	Phe	Thr	Asp	Pro	Ser	Ser	Val	Asn	Glu	Lys	Lys	Arg	Arg
	-70				-65				-60						
Glu	Arg	Glu	Glu	Arg	Gln	Asn	Ile	Val	Leu	Trp	Arg	Gln	Pro	Leu	Ile
	-55				-50				-45					-40	
Thr	Leu	Gln	Tyr	Phe	Ser	Leu	Glu	Ile	Leu	Val	Ile	Leu	Lys	Glu	Trp
			-35						-30					-25	
Thr	Ser	Lys	Leu	Trp	His	Arg	Gln	Ser	Ile	Val	Val	Ser	Phe	Leu	Leu
			-20					-15					-10		
Leu	Leu	Ala	Gly	Leu	Ile	Ala	Thr	Tyr	Tyr	Val	Glu	Gly	Val	His	Gln
	-5					1			5						
Gln	Tyr	Val	Gln	Arg	Ile	Glu	Lys	Gln	Phe	Leu	Leu	Tyr	Ala	Tyr	Trp
10				15					20					25	
Ile	Gly	Leu	Gly	Ile	Leu	Ser	Ser	Val	Gly	Leu	Gly	Thr	Gly	Leu	His
			30					35						40	
Thr	Phe	Leu	Leu	Tyr	Leu	Gly	Pro	His	Ile	Ala	Ser	Val	Thr	Leu	Ala
		45					50					55			
Ala	Tyr	Glu	Cys	Asn	Ser	Val	Asn	Phe	Pro	Glu	Pro	Pro	Tyr	Pro	Asp
	60					65						70			
Gln	Ile	Ile	Cys	Pro	Asp	Glu	Glu	Gly	Thr	Glu	Gly	Thr	Ile	Ser	Leu
	75				80						85				
Trp	Ser	Ile	Ile	Ser	Lys	Val	Arg	Ile	Glu	Ala	Cys	Met	Trp	Gly	Ile
90					95				100					105	
Gly	Thr	Ala	Ile	Gly	Glu	Leu	Pro	Pro	Tyr	Phe	Met	Ala	Arg	Ala	Ala
				110				115					120		
Arg	Leu	Ser	Gly	Ala	Glu	Pro	Asp	Asp	Glu	Glu	Tyr	Gln	Glu	Phe	Glu
			125				130					135			
Glu	Met	Leu	Glu	His	Ala	Glu	Ser	Ala	Gln	Val	Arg	Thr	Val	Gly	Ile

	140		145		150
Glu	Asn Arg Thr Leu Tyr Phe	Phe Leu Lys Arg	Leu Leu Arg		
155		160		165	

<210> 474
 <211> 178
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 474

Met	Glu	Arg	Gln	Ser	Arg	Val	Met	Ser	Glu	Lys	Asp	Glu	Tyr	Gln	Phe
	-35						-30					-25			
Gln	His	Gln	Gly	Ala	Val	Glu	Leu	Leu	Val	Phe	Asn	Phe	Leu	Leu	Ile
	-20					-15					-10				
Leu	Thr	Ile	Leu	Thr	Ile	Trp	Leu	Phe	Lys	Asn	His	Arg	Phe	Arg	Phe
5					1				5					10	
Leu	His	Glu	Thr	Gly	Gly	Ala	Met	Val	Tyr	Gly	Leu	Xaa	Met	Gly	Leu
		15					20					25			
Ile	Leu	Xaa	Tyr	Ala	Thr	Ala	Pro	Thr	Asp	Ile	Glu	Ser	Gly	Xaa	Val
	30						35				40				
Tyr	Asp	Cys	Val	Lys	Leu	Thr	Phe	Ser	Pro	Ser	Thr	Leu	Leu	Val	Asn
	45					50				55					
Ile	Thr	Asp	Gln	Val	Tyr	Glu	Tyr	Lys	Tyr	Lys	Arg	Glu	Ile	Ser	Gln
60					65					70				75	
His	Xaa	Ile	Asn	Pro	His	Xaa	Gly	Asn	Ala	Ile	Leu	Glu	Lys	Met	Thr
			80					85						90	
Phe	Asp	Pro	Xaa	Ile	Phe	Phe	Asn	Val	Leu	Leu	Pro	Pro	Ile	Ile	Phe
		95						100					105		
His	Ala	Gly	Tyr	Ser	Leu	Lys	Lys	Arg	His	Phe	Phe	Gln	Asn	Leu	Gly
	110						115					120			
Ser	Ile	Leu	Thr	Tyr	Ala	Phe	Leu	Gly	Thr	Ala	Ile	Ser	Cys	Ile	Val
	125					130					135				
Ile	Gly														
140															

<210> 475
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 475

Met	Ser	Met	Gln	Phe	Leu	Phe	Lys	Met	Val	Ala	Leu	Cys	Cys	Cys	Leu
	-20					-15					-10				
Trp	Lys	Ile	Ser	Gly	Cys	Glu	Glu	Val	Pro	Leu	Thr	Tyr	Asn	Leu	Leu
-5					1				5					10	

Lys	Cys	Leu	Leu	Asp	Lys	Ala	His	Cys	Val	Leu	Leu	Thr	Pro	Cys	Gly
			15					20					25		
Tyr	Ile	Phe	Ser	Leu	Ile	Ser	Pro	Glu	Ile	Leu	Lys	Leu	Thr	Leu	Ile
		30					35					40			
Thr	Leu	Xaa	Ile	Leu	Leu	Ile	Leu	Lys	Asn	Leu	His	Leu	Leu	Trp	Leu
		45				50					55				
Thr	Val	Ser	Ser	Xaa	Cys	Val	His	Arg	Ser	Ser	Ala	Arg	Lys	Glu	Lys
60					65					70					75

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<210> 476
<211> 41
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -24...-1
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<400> 476

Met	His	Thr	Phe	Ala	Asn	Asp	Arg	Gly	Leu	Tyr	Arg	Ile	Leu	Leu	Leu
				-20					-15					-10	
His	Phe	Tyr	Cys	Leu	Leu	Arg	Ser	Ser	Glu	Tyr	Ile	Leu	Gly	Tyr	Lys
			-5					1				5			
Val	Leu	Gly	Val	Phe	Phe	Pro	Ile	Leu							
	10					15									

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<210> 477
<211> 113
<212> PRT
<213> Homo sapiens
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 $\gamma_{Au}^{Au}$  <220>
 $\gamma_{Au}^{Au}$  <221> SIGNAL
 $\gamma_{Au}^{Au}$  <222> -27...-1

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<400> 477

[illegible]

<210> 478
 <211> 250
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 478

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Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
      -15                      -10                      -5
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
      1                      5                      10
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
15                      20                      25                      30
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
      35                      40                      45
Lys Pro Arg Tyr Ile Xaa His Leu Gly Gln His Asn Leu Gln Lys Glu
      50                      55                      60
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
      65                      70                      75
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp Xaa Xaa Asn Asp Ile Met
      80                      85                      90
Leu Val Xaa Met Xaa Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
95                      100                      105                      110
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
      115                      120                      125
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
      130                      135                      140
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
      145                      150                      155
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
160                      165                      170
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
175                      180                      185                      190
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
      195                      200                      205
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
      210                      215                      220
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
      225                      230

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<210> 479
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 479

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Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val

```

-20		-15		-10
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile				
-5		1	5	10
Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu				
	15		20	25
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala				
	30	35	40	
Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp		50	55	
	45			
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val				
60		65	70	75
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg				
	80	85	90	
Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile				
	95	100	105	
Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn				
	110	115	120	
Gly Lys Val Lys Ser Phe Lys				
	125	130		

<210> 480
 <211> 239
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 480

Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu				
-25		-20	-15	-10
Leu Leu Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe				
	-5	1	5	
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg				
	10	15	20	
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe				
	25	30	35	
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu				
40		45	50	55
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys				
	60	65	70	
Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala				
	75	80	85	
Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Xaa Xaa Xaa Xaa Leu Xaa				
	90	95	100	
Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala				
	105	110	115	
Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe				
120		125	130	135
Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Xaa Xaa				
	140	145	150	
Xaa Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys				
	155	160	165	
Ser Phe Ile Phe Leu Xaa Ile Leu Cys Thr Met Ser Ile Arg Gln Asn				

170	175	180
Ile Gln Lys Ile Leu Gly	Leu Ala Pro Ser Arg	Ala Ala Thr Lys Gln
185	190	195
Ala Gly Gly Phe Leu Gly	Pro Pro Pro Pro Ser	Gly Lys Phe Ser
200	205	210

<210> 481
 <211> 208
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -92...-1

<400> 481

Met Arg Glu Pro Gln Lys Arg Thr Ala Thr Ile Ala Lys Xaa Xaa Ala	-90	-85	-80
Xaa Glu Gly Leu Arg Asp Pro Tyr Gly Arg Leu Cys Gly Ser Glu His	-75	-70	-65
Pro Arg Arg Pro Pro Glu Arg Pro Glu Glu Asp Pro Ser Thr Pro Glu	-60	-55	-50
Glu Ala Ser Thr Thr Pro Glu Glu Ala Ser Ser Thr Ala Gln Ala Gln	-40	-35	-30
Lys Pro Ser Val Pro Arg Ser Asn Phe Gln Gly Thr Lys Lys Ser Leu	-25	-20	-15
Leu Met Ser Ile Leu Ala Leu Ile Phe Ile Met Gly Asn Ser Ala Lys	-10	-5	1
Glu Ala Leu Val Trp Lys Val Leu Gly Lys Leu Gly Met Gln Pro Gly	5	10	15
Arg Xaa His Ser Ile Phe Gly Asp Pro Lys Lys Ile Val Thr Glu Xaa	25	30	35
Phe Val Arg Arg Gly Tyr Leu Ile Tyr Xaa Pro Val Pro Arg Xaa Ser	40	45	50
Pro Val Glu Tyr Xaa Phe Phe Trp Gly Pro Arg Ala His Val Glu Ser	55	60	65
Ser Xaa Leu Lys Xaa Xaa His Phe Val Ala Arg Val Arg Asn Arg Cys	70	75	80
Ser Lys Asp Trp Pro Cys Asn Tyr Asp Trp Asp Ser Asp Asp Ala	85	90	95
Glu Val Glu Ala Ile Leu Asn Ser Gly Ala Xaa Gly Tyr Ser Ala Pro	105	110	115

<210> 482
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 482

Met	Asn	Val	Gly	Thr	Ala	His	Xaa	Xaa	Val	Asn	Pro	Asn	Thr	Arg	Val
			-35						-30					-25	
Met	Asn	Ser	Arg	Gly	Ile	Trp	Leu	Ser	Tyr	Val	Leu	Ala	Ile	Gly	Leu
			-20					-15					-10		
Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
		-5					1				5				
Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
10					15					20				25	
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
			30					35						40	
Arg	Leu	Leu	Thr	His	Trp										
			45												

<210> 483
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

Met	Arg	Thr	Leu	Phe	Gly	Ala	Val	Arg	Ala	Pro	Phe	Ser	Ser	Leu	Thr
		-25					-20				-15				
Leu	Leu	Leu	Ile	Thr	Pro	Ser	Pro	Ser	Pro	Leu	Leu	Phe	Asp	Arg	Gly
	-10				-5				1					5	
Leu	Ser	Leu	Arg	Ser	Ala	Met	Ser								
			10												

<210> 484
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

Met	Leu	Gly	Phe	Phe	Leu	Phe	Leu	Ser	Phe	Val	Leu	Met	Tyr	Asp	Gly
	-15				-10					-5					
Leu	Arg	Leu	Phe	Gly	Ile	Leu	Ser	Thr	Cys	Arg	Val	His	His	Thr	Met
1			5					10				15			
Asn	Gln	Phe	Leu	Ile	Asp	Ile	Ser	Ser	Phe	Thr	Ser	Arg	Val	Lys	Lys
		20					25					30			
Lys	Ile	Phe	Leu	Phe	Tyr	Ala	Phe	Xaa	Gly	Cys	Xaa	Phe	Gln	Ser	Ala
	35					40					45				
Thr															

<210> 485

<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -55..-1

<400> 485

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Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
-55                      -50                      -45                      -40
Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
                      -35                      -30                      -25
Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
                      -20                      -15                      -10
Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
                      -5                      1                      5
Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
10                      15                      20                      25
Leu Pro Thr Met Thr Ala Phe Ala Ser Gly Leu Gly Gly Glu Gly Xaa
                      30                      35                      40
Xaa Cys Val Cys Ser Asn Phe Thr Glu Gly Pro His Leu Glu Gly Arg
                      45                      50                      55
Pro Asp Gly Asp His Ser Gly Pro Ser Glu Leu Leu Thr Gln Gly Trp
60                      65                      70
Ala Leu
75

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<210> 486
<211> 209
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84..-1

<400> 486

```

Met Val Asn Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu
                      -80                      -75                      -70
Met Leu Val Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr
                      -65                      -60                      -55
Ser Asp Thr Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly
                      -50                      -45                      -40
Thr Cys Phe Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu
-35                      -30                      -25
Ala Tyr Leu Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu
-20                      -15                      -10                      -5
Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr
1                      5                      10
Asn Ile His Leu Arg Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly
15                      20                      25
Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val
30                      35                      40
Gly Pro Thr Xaa Arg Xaa Leu Leu Cys Gly Thr Leu Ala Ala Leu His

```

45					50					55					60
Met	Leu	Phe	Leu	Leu	Tyr	Leu	His	Phe	Ala	Tyr	His	Lys	Xaa	Val	Xaa
			65						70					75	
Gly	Ile	Leu	Asp	Thr	Leu	Glu	Gly	Pro	Asn	Ile	Pro	Pro	Ile	Gln	Arg
			80					85					90		
Val	Pro	Arg	Asp	Ile	Pro	Ala	Met	Leu	Pro	Ala	Ala	Arg	Leu	Pro	Thr
		95					100					105			
Thr	Val	Leu	Asn	Ala	Thr	Ala	Lys	Ala	Val	Ala	Val	Thr	Leu	Gln	Ser
	110					115					120				
His															
125															

<210> 487
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 487															
Met	Gly	Trp	Gln	Arg	Trp	Trp	Cys	Phe	His	Leu	Gln	Ala	Glu	Ala	Ser
		-15					-10					-5			
Ala	His	Pro	Pro	Gln	Gly	Leu	Gln	Ala	Gln	Phe	Ser	Cys	Cys	Pro	Trp
	1				5					10					15
Val	Gly	Ile	Cys												

<210> 488
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 488															
Met	Met	Ser	Ser	Glu	Leu	Arg	Arg	Asn	Pro	His	Phe	Leu	Lys	Ser	Asn
				-25				-20						-15	
Leu	Phe	Leu	Gln	Leu	Leu	Val	Ser	His	Glu	Ile	Val	Cys	Ala	Thr	Glu
			-10					-5				1			
Thr	Val	Thr	Thr	Asn	Phe	Leu	Arg	His	Glu	Lys	Ala				
	5					10					15				

<210> 489
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -52...-1

<400> 489

Met	Glu	His	Tyr	Arg	Lys	Ala	Gly	Ser	Val	Glu	Leu	Pro	Ala	Pro	Ser
		-50					-45					-40			
Pro	Met	Pro	Gln	Leu	Pro	Pro	Asp	Thr	Leu	Glu	Met	Arg	Val	Arg	Asp
	-35					-30				-25					
Gly	Ser	Lys	Ile	Arg	Asn	Leu	Leu	Gly	Leu	Ala	Leu	Gly	Arg	Leu	Glu
-20					-15					-10					-5
Gly	Gly	Ser	Ala	Arg	His	Val	Val	Phe	Ser	Gly	Ser	Gly	Arg	Ala	Ala
				1				5					10		
Gly	Lys	Ala	Val	Ser	Cys	Ala	Glu	Ile	Val	Lys	Arg	Arg	Val	Pro	Gly
	15						20					25			
Leu	His	Gln	Leu	Thr	Lys	Leu	Xaa	Phe	Leu	Gln	Thr	Glu	Asp	Ser	Trp
	30					35					40				
Val	Pro	Xaa	Ser	Pro	Asp	Thr	Gly	Leu	Xaa	Pro	Leu	Thr	Val	Arg	Arg
45					50					55					60
His	Val	Pro	Ala	Xaa	Trp	Val	Leu	Leu	Xaa	Arg	Asp	Pro	Leu	Asp	Pro
				65					70					75	
Asn	Glu	Cys	Gly	Tyr	Gln	Pro	Pro	Gly	Ala	Pro	Pro	Gly	Leu	Gly	Ser
			80					85					90		
Met	Pro	Ser	Ser	Ser	Cys	Gly	Pro	Arg	Ser	Xaa	Lys	Arg	Ala	Xaa	Xaa
		95					100					105			
Thr	Arg	Ser													
		110													

<210> 490

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 490

Met	His	Gly	Phe	Glu	Ile	Ile	Ser	Leu	Lys	Glu	Glu	Ser	Pro	Leu	Gly
		-45					-40					-35			
Lys	Val	Ser	Gln	Gly	Pro	Leu	Phe	Asn	Val	Thr	Ser	Gly	Ser	Ser	Ser
	-30					-25					-20				
Pro	Val	Thr	Trp	Leu	Gly	Leu	Leu	Ser	Phe	Gln	Asn	Leu	His	Cys	Phe
-15					-10					-5				1	
Pro	Asp	Leu	Pro	Thr	Glu	Met	Pro	Leu	Xaa	Ala	Lys	Gly	Xaa	Asn	Thr
		5						10					15		

<210> 491

<211> 218

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -50...-1

<400> 491

Met	His	His	Gly	Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys
-50					-45					-40					-35
Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala
				-30					-25					-20	
Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly
			-15					-10					-5		
Ser	Ala	Ser	Ile	Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser
	1				5					10					
Ser	Gln	Asp	Leu	Ser	Gly	Gln	Thr	Ala	Lys	Lys	Tyr	Ala	Val	Ser	Ser
15					20					25					30
Arg	His	Asn	Val	Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Xaa	Lys	Gln
				35					40					45	
Xaa	Leu	Lys	Val	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Xaa	Gln	Asp	Leu	Lys
			50					55					60		
Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	Lys	Gly	Ser	Glu	Asn	Ser
			65				70					75			
Gln	Pro	Glu	Glu	Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Xaa	Gly	Gly	Asp
	80					85					90				
Arg	Lys	Val	Glu	Xaa	Xaa	Met	Lys	Lys	His	Gly	Ser	Xaa	His	Met	Gly
	95				100					105					110
Phe	Pro	Xaa	Asn	Leu	Xaa	Asn	Gly	Ala	Thr	Ala	Asp	Asn	Gly	Asp	Asp
				115					120					125	
Gly	Leu	Ile	Pro	Pro	Xaa	Lys	Xaa	Xaa	Thr	Pro	Glu	Ser	Xaa	Gln	Phe
			130				135						140		
Pro	Asp	Thr	Glu	Asn	Glu	Gln	Tyr	His	Arg	Asp	Phe	Ser	Gly	His	Pro
			145				150					155			
Xaa	Phe	Pro	Thr	Thr	Leu	Pro	Ile	Lys	Gln						
	160					165									

<210> 492

<211> 216

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 492

Met	Val	Cys	Val	Leu	Val	Leu	Ala	Ala	Ala	Ala	Gly	Ala	Val	Ala	Val
-15					-10					-5					1
Phe	Leu	Ile	Leu	Arg	Ile	Trp	Val	Val	Leu	Arg	Ser	Met	Asp	Val	Thr
			5				10					15			
Pro	Arg	Glu	Ser	Leu	Ser	Ile	Leu	Val	Val	Ala	Gly	Ser	Gly	Gly	His
			20			25						30			
Thr	Thr	Glu	Ile	Leu	Arg	Leu	Gly	Ser	Leu	Ser	Asn	Ala	Tyr	Ser	
			35			40				45					
Pro	Arg	His	Tyr	Val	Ile	Ala	Asp	Thr	Asp	Glu	Met	Ser	Ala	Asn	Lys
50					55					60					65
Ile	Asn	Ser	Phe	Glu	Leu	Xaa	Arg	Xaa	Asp	Arg	Xaa	Pro	Ser	Asn	Met
				70					75					80	
Xaa	Thr	Lys	Tyr	Tyr	Ile	His	Arg	Ile	Pro	Xaa	Ser	Arg	Glu	Val	Gln

			85					90					95				
Gln	Ser	Trp	Pro	Ser	Thr	Val	Xaa	Thr	Thr	Leu	His	Ser	Met	Trp	Leu		
			100					105					110				
Ser	Xaa	Pro	Leu	Ile	His	Arg	Val	Lys	Pro	Xaa	Leu	Val	Leu	Cys	Asn		
			115				120					125					
Gly	Pro	Gly	Thr	Cys	Val	Pro	Ile	Cys	Val	Ser	Ala	Leu	Leu	Leu	Gly		
130					135					140					145		
Ile	Leu	Gly	Ile	Lys	Lys	Val	Ile	Ile	Val	Tyr	Val	Glu	Ser	Ile	Cys		
				150					155					160			
Arg	Val	Lys	Thr	Leu	Ser	Met	Ser	Gly	Lys	Ile	Leu	Phe	His	Leu	Ser		
			165					170					175				
Asn	Tyr	Phe	Ile	Val	Gln	Trp	Pro	Ala	Leu	Lys	Glu	Lys	Tyr	Pro	Lys		
		180					185					190					
Ser	Val	Tyr	Leu	Gly	Arg	Ile	Val										
		195				200											

<210> 493

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 493

Met	Pro	Leu	Gly	Ala	Arg	Ile	Leu	Phe	His	Gly	Val	Phe	Tyr	Ala	Gly		
				-15					-10					-5			
Gly	Phe	Ala	Ile	Val	Tyr	Tyr	Leu	Ile	Gln	Lys	Phe	His	Ser	Arg	Thr		
			1				5					10					
Leu	Tyr	Tyr	Lys	Leu	Ala	Val	Glu	Gln	Leu	Gln	Xaa	His	Pro	Glu	Ala		
	15					20					25						
Gln	Glu	Ala	Leu	Gly	Pro	Pro	Leu	Asn	Ile	His	Tyr	Leu	Lys	Leu	Ile		
30					35					40					45		
Asp	Arg	Glu	Asn	Phe	Val	Asp	Ile	Val	Xaa	Ala	Lys	Leu	Lys	Ile	Pro		
			50						55					60			
Val	Ser	Gly	Ser	Lys	Ser	Glu	Gly	Leu	Leu	Tyr	Val	His	Ser	Ser	Arg		
			65					70					75				
Gly	Gly	Pro	Phe	Gln	Arg	Trp	His	Leu	Asp	Glu	Val	Phe	Leu	Glu	Leu		
		80					85					90					
Lys	Asp	Gly	Gln	Gln	Ile	Pro	Val	Phe	Lys	Leu	Ser	Gly	Glu	Asn	Gly		
	95					100					105						
Asp	Glu	Val	Lys	Lys	Glu												
110					115												

<210> 494

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 494

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Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
  -15                      -10                      -5
Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
 1                      5                      10                      15
Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly
                20                      25                      30
Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln Ser Thr
                35                      40                      45
Glu Gln Leu Ala Xaa Leu Lys Lys Xaa His Glu Glu Glu Ile Val His
                50                      55                      60
His Arg Glu Gly Asp
65

```

<210> 495

<211> 292

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 495

```

Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe
                -25                      -20                      -15
Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr
                -10                      -5                      1
Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr
 5                      10                      15
Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr
20                      25                      30                      35
Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu
                40                      45                      50
Leu Phe Leu His Val Tyr Glu Phe Asp Glu Xaa Met Phe Pro Lys Asn
                55                      60                      65
Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Xaa His
                70                      75                      80
Cys Xaa Val Cys Asn Trp Cys Val His Arg Phe Xaa His His Cys Val
 85                      90                      95
Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg Xaa Phe Leu Ile
100                      105                      110                      115
Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser
                120                      125                      130
Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu
                135                      140                      145
Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met Asp Thr Val Phe
                150                      155                      160
Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu
                165                      170                      175
Gly Phe Val Val Val Leu Xaa Phe Leu Leu Gly Gly Tyr Leu Leu Phe
180                      185                      190                      195
Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg
                200                      205                      210

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Xaa Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro
 215 220 225
 Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His Gly Leu Arg
 230 235 240
 Xaa Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg
 245 250 255
 Lys Lys Gln Glu
 260

<210> 496
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56...-1

<400> 496

Met Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser
 -55 -50 -45
 Cys Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser
 -40 -35 -30 -25
 Ser Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro
 -20 -15 -10
 Gly Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Xaa Leu Thr Gly
 -5 1 5
 Pro Xaa Thr Asp Gly Ile Pro Phe Ala Leu Xaa Ser Ala Ala Gly Pro
 10 15 20
 Phe Cys Ala Ser Phe Pro Ser Gly Xaa Leu Ser Pro Pro Gly Pro Leu
 25 30 35 40
 Pro Gly Val Arg Gly Leu Pro Leu Pro Ser Val Phe Tyr Ser Cys Gly
 45 50 55
 Ala His Pro Lys Val Leu Lys Val Ala Leu
 60 65

<210> 497
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 497

Met Leu Xaa Leu Ser Arg Ala Thr Lys Xaa Gly Arg Ala Arg Trp Leu
 -25 -20 -15
 Met Pro Val Ile Pro Ala Leu Gln Glu Ala Xaa Ala Gly Gly Ser Arg
 -10 -5 1
 Gly Gln Glu Phe Glu Thr Ser Leu Ala Asn Met Glu Thr Glu Ala Gly
 5 10 15 20
 Glu Leu Leu Lys Pro Arg Arg Arg Arg Leu Gln

25

30

<210> 498
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 498
Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
5 10 15
Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
20 25 30 35
Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
Arg Arg Ser Ser Cys His Leu Glu Cys Xaa Val Ile Phe Leu Leu Gly
 70 75 80
Arg Gln Leu
85

<210> 499
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 499
Met His Leu Leu Ser Asn Trp Ala Asn Pro Ala Ser Ser Arg Arg Pro
 -10 -5 1
Ser Met Ala Ala Ser Gly Thr Ser Trp Ile Ser Ser Thr Leu Ala His
5 10 15
Ser Leu Ser Leu Arg Asp Val Ser Glu Arg Leu Cys Ser Cys Trp Arg
20 25 30 35
Thr Ile Ser Met Gly Pro Cys Ala Arg Gly Ser Pro Met Asn Ser Ser
 40 45 50
Gly Val His Arg Lys Ser Ser Arg Leu Phe Tyr Ile Arg Thr Pro Met
 55 60 65
Arg Arg Ser Ser Cys His Leu Xaa Cys Gln Val Ile Phe Leu Leu Gly
 70 75 80
Arg Gln Leu
85

<210> 500
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 500
Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
-25 -20 -15 -10
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
-5 1 5
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
10 15 20
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
25 30 35
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
40 45 50 55
Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
60 65 70
Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
75 80

<210> 501
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 501
Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1
Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15
Gln Gly Arg Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30
His Pro Asp Asp Glu Ala Met Phe Phe Ala Pro Thr Val Leu Gly Leu
35 40 45
Ala Arg Leu Arg His Trp Val Tyr Leu Leu Cys Phe Ser Ala Gly Asn
50 55 60 65
Tyr Tyr Asn Gln Gly Glu Thr Arg Lys Lys Glu Leu Leu Gln Ser Cys
70 75 80
Asp Val Leu Gly Ile Pro Leu Ser Ser Val Met Ile Ile Asp Asn Arg
85 90 95
Asp Phe Pro Xaa Asp Pro Gly Met Gln Trp Asp Thr Xaa His Val Ala
100 105 110
Xaa Val Leu Leu Gln His Ile Glu Val Asn Gly Ile Asn Leu Val Val
115 120 125
Thr Phe Asp Ala Gly Gly Xaa Ser Gly His Ser Asn His Ile Ala Leu

130		135		140		145									
Tyr	Ala	Ala	Val	Arg	Lys	Leu	Glu	Gly	Gln	Ile	Cys	Lys	Pro	Cys	Gly
				150					155					160	
Thr	Gly	Gln	Asp	Phe	Lys	Glu									
			165												

<210> 502
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 502															
Met	Glu	Ala	Met	Trp	Leu	Leu	Cys	Val	Ala	Leu	Ala	Val	Leu	Ala	Trp
-15					-10					-5					1
Gly	Phe	Leu	Trp	Val	Trp	Asp	Ser	Ser	Glu	Arg	Met	Lys	Ser	Arg	Glu
			5				10					15			
Gln	Gly	Xaa	Arg	Leu	Gly	Ala	Glu	Ser	Arg	Thr	Leu	Leu	Val	Ile	Ala
		20				25					30				
His	Pro	Asp	Asp	Glu	Ala	Met	Phe	Phe	Ala	Pro	Thr	Val	Leu	Gly	Leu
	35					40				45					
Ala	Arg	Leu	Arg	His	Trp	Val	Tyr	Leu	Leu	Cys	Phe	Ser	Ala	Val	Phe
50					55					60					65
Arg	Arg	Glu	Leu	Ser	Glu	Tyr	Thr	Glu	Xaa	Leu	Thr	Ser	Glu	Pro	Leu
				70					75					80	
Xaa	Ala														

<210> 503
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -57..-1

<400> 503															
Met	Asp	Val	Thr	Gly	Asp	Glu	Glu	Glu	Glu	Ile	Lys	Gln	Glu	Ile	Asn
	-55					-50					-45				
Met	Leu	Lys	Lys	Tyr	Ser	His	His	Arg	Asn	Ile	Ala	Thr	Tyr	Tyr	Gly
	-40					-35					-30				
Ala	Phe	Ile	Lys	Lys	Asn	Pro	Pro	Gly	Met	Asp	Asp	Gln	Leu	Trp	Leu
-25					-20					-15					-10
Val	Met	Glu	Phe	Cys	Gly	Ala	Gly	Ser	Val	Thr	Asp	Leu	Ile	Lys	Asn
			-5					1				5			
Thr	Lys	Gly	Asn	Thr	Leu	Lys	Glu	Glu	Trp	Ile	Ala	Tyr	Ile	Cys	Xaa
	10					15					20				
Glu	Ile	Leu	Arg	Gly	Leu	Xaa	His	Leu	His	Gln	His	Lys	Val	Ile	His
	25				30					35					
Arg	Xaa	Ile	Lys	Gly	Gln	Asn	Val	Leu	Leu	Thr	Glu	Asn	Ala	Glu	Val

40		45		50		55									
Lys	Leu	Val	Asp	Phe	Gly	Xaa	Xaa	Ala	Gln	Leu	Asp	Arg	Thr	Val	Gly
				60					65					70	
Arg	Xaa	Asn	Thr	Phe	Ile	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Xaa	Val
			75					80					85		
Ile	Ala	Cys	Asp	Glu	Asn	Pro	Xaa	Ala	Thr	Tyr	Asp	Phe	Lys	Xaa	Asp
		90					95					100			
Leu	Trp	Ser	Leu	Gly	Ile	Thr	Ala	Ile	Glu	Met	Ala	Glu	Gly	Leu	Pro
	105					110					115				
Leu	Ser	Val	Thr	Cys	Thr	Pro									
120					125										

<210> 504
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 504
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
-10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
35 40 45 50
Leu Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
70 75 80
Xaa His Gln Glu Met Val Leu Ile Leu Ser Arg His Pro Trp Ile Leu
85 90 95
Trp Ile Thr Glu Leu Thr Ile Phe Thr Trp Ser Gly Leu Lys Asn Cys
100 105 110
Ser Leu Cys Glu Asn Glu Leu Trp Thr Ser Leu Tyr
115 120 125

<210> 505
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 505
Met Ala Ala Leu Val Thr Val Leu Phe Thr Gly Val Arg Arg Leu His
-10 -5 1

Cys	Ser	Ala	Xaa	Leu	Gly	Arg	Ala	Ala	Ser	Gly	Xaa	Tyr	Ser	Arg	Asn
	5						10					15			
Trp	Leu	Pro	Thr	Pro	Pro	Ala	Thr	Gly	Pro	Leu	Pro	Ser	Ser	Gln	Thr
20						25					30				
Gly	His	Met	Arg	Met	Ala	Ala	Leu	Leu	Pro	Gln					
35					40					45					

<210> 506
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

Met	Gly	Pro	Tyr	Asn	Val	Ala	Val	Pro	Ser	Asp	Val	Ser	His	Ala	Arg
-35						-30					-25				
Phe	Tyr	Phe	Leu	Phe	His	Arg	Pro	Leu	Arg	Leu	Leu	Asn	Leu	Leu	Ile
20					-15					-10					-5
Leu	Ile	Glu	Gly	Ser	Val	Val	Phe	Tyr	Gln	Leu	Tyr	Ser	Leu	Leu	Arg
				1				5				10			
Ser	Glu	Lys	Trp	Asn	His	Thr	Leu	Ser	Met	Ala	Leu	Ile	Leu	Phe	Cys
	15						20				25				
Asn	Tyr	Tyr	Val	Leu	Phe	Lys	Leu	Leu	Arg	Asp	Arg	Xaa	Xaa	Leu	Gly
30						35				40					
Arg	Ala	Tyr	Ser	Tyr	Pro	Leu	Asn	Ser	Tyr	Glu	Leu	Lys	Ala	Asn	Xaa
45					50					55					60
Ala	Ala	Ser	Xaa	Gln											
				65											

<210> 507
 <211> 341
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

Met	Arg	Lys	Val	Val	Leu	Ile	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Leu
-55					-50					-45					-40
Ala	Leu	Cys	Lys	Arg	Leu	Leu	Ala	Glu	Asp	Asp	Glu	Leu	His	Leu	Cys
				-35					-30						-25
Leu	Ala	Cys	Arg	Asn	Met	Ser	Lys	Ala	Glu	Ala	Val	Cys	Ala	Ala	Leu
			-20					-15					-10		
Leu	Ala	Ser	His	Pro	Thr	Ala	Glu	Val	Thr	Ile	Val	Gln	Val	Asp	Val
	-5					1				5					
Ser	Asn	Leu	Gln	Ser	Phe	Phe	Arg	Ala	Ser	Lys	Glu	Leu	Lys	Gln	Arg
10				15					20					25	
Phe	Gln	Arg	Leu	Asp	Cys	Ile	Tyr	Leu	Asn	Ala	Gly	Ile	Met	Pro	Asn

[illegible]

~~SECRET~~ <210> 508

Q211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 508

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
		-40					-35					-30			
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
		-25				-20					-15				
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Ala	Ile	Ile
					-5					1				5	
Leu	Gln	Xaa	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
			10					15					20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Xaa	Tyr	Leu	Lys	Ile	Xaa	Lys
		25					30					35			
Gly	Asp	Gly	Gly	Ser	Gly	Ser	Lys	Gly	Arg	Pro	Xaa	Xaa	Gln	Thr	Glu

40		45		50
Xaa	Phe	Leu	Cys	Ile
55		60		65

<210> 509
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 509
 Met Glu Glu Ile Ser Ser Pro Leu Val Glu Phe Val Lys Val Leu Cys
 -25 -20 -15
 Thr Asn Gln Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala
 -10 -5 1 5
 Ser Val Arg Cys Val Glu Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser
 10 15 20
 Lys His Leu Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp
 25 30 35
 Phe Thr Phe Cys Leu Glu Phe Ser Arg His Arg Cys Gln Leu Thr Glu
 40 45 50

<210> 510
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44...-1

<400> 510
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys Ile
 -40 -35 -30
 Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala Gly Ile
 -25 -20 -15
 Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala Val Val Tyr
 -10 -5 1
 Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys Gly Val Phe
 5 10 15 20
 Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn Ala Gln Val
 25 30 35
 Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr Gly Ala Arg
 40 45 50
 Val Trp Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser Leu Ile Ala
 55 60 65
 Ser Met Trp Ile Leu Phe Gly Ala Tyr Val Thr Gln Asn Thr Asp Val
 70 75 80
 Tyr Pro Gly Leu Ala Val Phe Phe Gln Asn Ala Leu Ile Phe Phe Ser
 85 90 95 100

Thr Leu Ile Tyr Lys Phe Gly Arg Thr Glu Glu Leu Trp Thr
105 110

<210> 511
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 511

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
-25 -20 -15
Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
-10 -5 1
Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
5 10 15 20
Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
25 30 35
Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
40 45 50
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
55 60 65
Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
70 75 80
Thr Asp Thr Gly Ser His Glu Ser Gly Tyr Gln Ser Cys Ser Pro Gly
85 90 95 100
Ile Trp

<210> 512
<211> 199
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -62...-1

<400> 512

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
-60 -55 -50
Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
-45 -40 -35
Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val
-30 -25 -20 -15
Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
-10 -5 1
Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu
5 10 15
Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro
20 25 30

Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	Leu	Ala	Gly	Glu	Val	Thr	Lys
35					40					45					50
Thr	Ile	Gly	Asn	Asn	Gly	Asn	Gln	Ser	His	Lys	Met	Thr	Thr	Ser	Arg
			55						60					65	
Cys	Val	Arg	Leu	Met	Leu	Ile	Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val
			70					75					80		
Trp	Ile	Ser	Glu	Gln	Pro	Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr
		85					90					95			
Met	Pro	Thr	Trp	Ala	Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg
	100					105					110				
Ile	Glu	Asn	Phe	Lys	Ser	Gly	Val	Asp	Ala	Xaa	Ser	Ser	Tyr	Phe	Lys
115					120					125					130
Ile	Phe	Lys	Thr	Lys	His	Asp									
				135											

<210> 513

<211> 180

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 513

Met	Asn	Thr	Val	Leu	Ser	Arg	Ala	Asn	Ser	Leu	Phe	Ala	Phe	Ser	Leu
-25					-20					-15					-10
Ser	Val	Met	Ala	Ala	Leu	Thr	Phe	Gly	Cys	Phe	Ile	Xaa	Thr	Ala	Phe
			-5					1				5			
Lys	Asp	Arg	Ser	Val	Pro	Val	Arg	Leu	His	Val	Ser	Arg	Ile	Met	Leu
	10					15						20			
Lys	Asn	Val	Glu	Asp	Phe	Thr	Gly	Pro	Arg	Glu	Arg	Ser	Asp	Leu	Gly
	25					30					35				
Phe	Ile	Thr	Phe	Asp	Ile	Thr	Ala	Asp	Leu	Glu	Asn	Ile	Phe	Asp	Trp
40					45					50					55
Asn	Val	Lys	Gln	Leu	Phe	Leu	Tyr	Leu	Ser	Ala	Glu	Tyr	Ser	Thr	Lys
			60						65					70	
Asn	Asn	Ala	Leu	Asn	Gln	Xaa	Val	Leu	Trp	Asp	Lys	Ile	Val	Leu	Arg
		75						80					85		
Gly	Asp	Asn	Pro	Lys	Leu	Leu	Leu	Lys	Asp	Met	Lys	Thr	Lys	Tyr	Phe
		90					95					100			
Phe	Phe	Asp	Asp	Gly	Asn	Gly	Leu	Xaa	Gly	Asn	Arg	Asn	Val	Thr	Leu
	105					110					115				
Thr	Leu	Ser	Trp	Asn	Val	Val	Pro	Asn	Ala	Gly	Ile	Leu	Pro	Leu	Val
120					125					130					135
Thr	Gly	Ser	Gly	His	Val	Ser	Val	Pro	Phe	Pro	Asp	Thr	Tyr	Glu	Ile
				140					145					150	
Thr	Lys	Ser	Tyr												
			155												

<210> 514

<211> 120

<212> PRT

<213> Bos taurus

<400> 514

Met	Met	Thr	Gly	Arg	Gln	Gly	Arg	Ala	Thr	Phe	Gln	Phe	Leu	Pro	Asp
1				5					10					15	
Glu	Ala	Arg	Ser	Leu	Pro	Pro	Pro	Lys	Leu	Thr	Asp	Pro	Arg	Leu	Ala
			20					25					30		
Phe	Val	Gly	Phe	Leu	Gly	Tyr	Cys	Ser	Gly	Leu	Ile	Asp	Asn	Ala	Ile
			35				40					45			
Arg	Arg	Arg	Pro	Val	Leu	Leu	Ala	Gly	Leu	His	Arg	Gln	Leu	Leu	Tyr
			50				55					60			
Ile	Thr	Ser	Phe	Val	Phe	Val	Gly	Tyr	Tyr	Leu	Leu	Lys	Arg	Gln	Asp
65					70					75				80	
Tyr	Met	Tyr	Ala	Val	Arg	Asp	His	Asp	Met	Phe	Ser	Tyr	Ile	Lys	Ser
				85					90					95	
His	Pro	Glu	Asp	Phe	Pro	Glu	Lys	Asp	Lys	Lys	Thr	Tyr	Gly	Glu	Val
			100					105					110		
Phe	Glu	Glu	Phe	His	Pro	Val	Arg								
			115				120								

<210> 515

<211> 1082

<212> DNA

<213> Homo sapiens

<400> 515

gatccagac	ctcggcttgc	agtagtggtta	gactgaagat	aaagtaagt	ctgtttgggc	60
taacaggatc	tctcttgcga	gtctgcagcc	caggacgctg	attccagcag	cgccttaccg	120
cgagcccga	agattcacta	tggtgaaaat	cgccttcaat	accctaccg	ccgtgcaaaa	180
ggaggaggcg	cggcaagacg	tggaggccct	cctgagccgc	acggtcagaa	ctcagatact	240
gaccggcaag	gagctccgag	ttgccaccca	ggaaaaagag	ggctcctctg	ggagatgtat	300
gcttactctc	ttaggccttt	cattcatctt	ggcaggactt	attgttggtg	gagcctgcat	360
ttacaagtac	ttcatgcca	agagcaccat	ttaccgtgga	gagatgtgct	tttttgattc	420
tgaggatcct	gcaaattccc	ttcgtggagg	agagcctaac	ttcctgcctg	tgactgagga	480
ggctgacatt	cgtgaggatg	acaacattgc	aatcattgat	gtgcctgtcc	ccagtttctc	540
tgatagtgac	cctgcagcaa	ttattcatga	ctttgaaaag	ggaatgactg	cttacctgga	600
cttgttgctg	gggaactgct	atctgatgcc	cctcaatact	tctattgtta	tgctccaaa	660
aaatctggta	gagctctttg	gcaaactggc	gagtggcaga	tatctgcctc	aaacttatgt	720
ggttcgagaa	gacctagtgt	ctgtggagga	aattcgtgat	gttagtaacc	ttggcatctt	780
tatttaccaa	ctttgcaata	acagaaaagtc	cttccgcctt	cgtcgcagag	acctcttgct	840
gggtttcaac	aaacgtgcca	ttgataaatg	ctggaagatt	agacacttcc	ccaacgaatt	900
tattgttgag	accaagatct	gtcaagagta	agaggcaaca	gatagagtgt	ccttggtaat	960
aagaagtcag	agatttaca	tatgacttta	acattaaggt	ttatgggata	ctcaagatat	1020
ttactcatgc	atttactcta	ttgcttatgc	cgtaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1080
aa						1082

<210> 516

<211> 559

<212> DNA

<213> Homo sapiens

<400> 516

ctgctccagc	gctgacgccg	agccatggcg	gacgaggagc	ttgaggcgct	gaggagacag	60
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aggctggccg agctgcaggc caaacacggg gatcctggtg atgcggccca acaggaagca 120
aagcacaggg aagcagaaat gagaaacagt atcttagccc aagttctgga tcagtcggcc 180
cgggccaggt taagtaactt agcacttgta aagcctgaaa aaactaaagc agtagagaat 240
taccttatac agatggcaag atatggacaa ctaagtgaga aggtatcaga acaaggttta 300
atagaaatcc ttaaaaaagt aagccaacaa acagaaaaga caacaacagt gaaattcaac 360
agaagaaaag taatggactc tgatgaagat gacgattatt gaactacaag tgctcacaga 420
ctagaactta acggaacaag tctaggacag aagttaagat ctgattattt actttgttta 480
ttgtctatat gcctttttaa aaaataaaact tgttatgcaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa aaaaaaaaaa 559

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<210> 517
 <211> 110
 <212> PRT
 <213> Homo sapiens

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<400> 517
Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp Tyr
1          5          10          15
Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr Val
          20          25          30
His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu
          35          40          45
Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His
          50          55          60
Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro
          65          70          75          80
Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys
          85          90          95
Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Asp Val Glu
          100          105          110

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<210> 518
 <211> 4544
 <212> DNA
 <213> Homo sapiens

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<400> 518
ccgagaaggg cttcaggacg cgggaggcgc acttgcttca agtcgcgggc gtgggaacgg 60
ggttgcaaaa cggggccttt ttatccgggc ttgcttccgg cgtcatggct caaagggcct 120
tcccgaatcc ttatgctgat tataacaaat ccctggccga aggctacttt gatgctgccg 180
ggaggctgac tcctgagttc tcacaacgct tgaccaataa gattcggggag cttcttcagc 240
aaatggagag aggcctgaaa tcagcagacc ctccggatgg caccggttac actggctggg 300
cagggtattgc tgtgctttac ttacatcttt atgatgtatt tggggaccct gcctacctac 360
agttagcaca tggctatgta aagcaaagtc tgaactgctt aaccaagcgc tccatcacct 420
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